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NEWS	2		"Ask CAS" for self-help around the clock
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NEWS	4	JAN 27	A new search aid, the Company Name Thesaurus, available in CA/Caplus
NEWS	5	FEB 05	German (DE) application and patent publication number format changes
NEWS	6	MAR 03	MEDLINE and LMEDLINE reloaded
NEWS	7	MAR 03	MEDLINE file segment of TOXCENTER reloaded
NEWS	8	MAR 03	FRANCEPAT now available on STN
NEWS	9	MAR 29	Pharmaceutical Substances (PS) now available on STN
NEWS	10	MAR 29	WPIFV now available on STN
NEWS	11	MAR 29	No connect hour charges in WPIFV until May 1, 2004
NEWS	12	MAR 29	New monthly current-awareness alert (SDI) frequency in RAPRA
NEWS	13	APR 26	PROMT: New display field available
NEWS	14	APR 26	IFIPAT/IFIUDB/IFICDB: New super search and display field available
NEWS	15	APR 26	LITALERT now available on STN
NEWS	16	APR 27	NLDB: New search and display fields available
NEWS EXPRESS			MARCH 31 CURRENT WINDOWS VERSION IS V7.00A, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 26 APRIL 2004
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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 14:17:20 ON 29 APR 2004

=> file medline, uspatful, dgene, embase, wpids, jicst		
COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.63	0.63

FILE 'MEDLINE' ENTERED AT 14:18:46 ON 29 APR 2004

FILE 'USPATFULL' ENTERED AT 14:18:46 ON 29 APR 2004
CA INDEXING COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'DGENE' ENTERED AT 14:18:46 ON 29 APR 2004
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COPYRIGHT (C) 2004 THOMSON DERWENT

FILE 'JICST-EPLUS' ENTERED AT 14:18:46 ON 29 APR 2004
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=> s myelogenous leukemia
L1 22800 MYELOGENOUS LEUKEMIA

=> s myeloid cell proliferation
L2 142 MYELOID CELL PROLIFERATION

=> s "HOIPS I"
L3 18 "HOIPS I"

=> s l3 and l2
L4 0 L3 AND L2

=> s l3 and l1
L5 2 L3 AND L1

=> d l5 ti abs ibib tot

L5 ANSWER 1 OF 2 USPATFULL on STN
TI Human oncogene induced secreted protein I
AB The present invention relates to a novel protein, the Human Oncogene Induced Secreted Protein I ("HOIPS I") protein. In particular, isolated nucleic acid molecules are provided encoding the human HOIPS I protein. HOIPS I polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. Also provided are diagnostic methods for detecting abnormal cell proliferation and differentiation disorders and therapeutic methods for treating the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:221411 USPATFULL
TITLE: Human oncogene induced secreted protein I
INVENTOR(S): Olsen, Henrik S., Gaithersburg, MD, UNITED STATES
Ruben, Steven M., Olney, MD, UNITED STATES
PATENT ASSIGNEE(S): Human Genome Sciences, Inc. (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002119552	A1	20020829
APPLICATION INFO.:	US 2001-899917	A1	20010709 (9)
RELATED APPLN. INFO.:	Division of Ser. No. US 1997-994962, filed on 19 Dec 1997, PATENTED		

	NUMBER	DATE
PRIORITY INFORMATION:	US 1996-33869P	19961220 (60)
	US 1997-37388P	19970207 (60)
DOCUMENT TYPE:	Utility	

FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C., 1100 NEW
YORK AVENUE, N.W., SUITE 600, WASHINGTON, DC,
20005-3934
NUMBER OF CLAIMS: 16
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 4 Drawing Page(s)
LINE COUNT: 2059
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 2 OF 2 USPATFULL on STN
TI Human oncogene induced secreted protein I
AB The present invention relates to a novel protein, the Human Oncogene
Induced Secreted Protein I ("HOIPS I") protein. In
particular, isolated nucleic acid molecules are provided encoding the
human HOIPS I protein. HOIPS I
polypeptides are also provided as are vectors, host cells and
recombinant methods for producing the same. Also provided are diagnostic
methods for detecting abnormal cell proliferation and differentiation
disorders and therapeutic methods for treating the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2001:147697 USPATFULL
TITLE: Human oncogene induced secreted protein I
INVENTOR(S): Olsen, Henrik S., Gaithersburg, MD, United States
Ruben, Steven M., Olney, MD, United States
PATENT ASSIGNEE(S): Human Genome Sciences, Inc., Rockville, MD, United
States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6284486	B1	20010904
APPLICATION INFO.:	US 1997-994962		19971219 (8)
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	GRANTED		
PRIMARY EXAMINER:	Carlson, Karen Cochrane		
LEGAL REPRESENTATIVE:	Sterne, Kessler, Goldstein & Fox P.L.L.C.		
NUMBER OF CLAIMS:	69		
EXEMPLARY CLAIM:	1		
NUMBER OF DRAWINGS:	4 Drawing Figure(s); 4 Drawing Page(s)		
LINE COUNT:	1994		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d his

(FILE 'HOME' ENTERED AT 14:17:20 ON 29 APR 2004)

FILE 'MEDLINE, USPATFULL, DGENE, EMBASE, WPIDS, JICST-EPLUS' ENTERED AT
14:18:46 ON 29 APR 2004

L1 22800 S MYELOGENOUS LEUKEMIA
L2 142 S MYELOID CELL PROLIFERATION
L3 18 S "HOIPS I"
L4 0 S L3 AND L2
L5 2 S L3 AND L1

=> d l3 ti abs ibib tot

L3 ANSWER 1 OF 18 USPATFULL on STN
TI Human oncogene induced secreted protein I
AB The present invention relates to a novel protein, the Human Oncogene
Induced Secreted Protein I ("HOIPS I") protein. In
particular, isolated nucleic acid molecules are provided encoding the
human HOIPS I protein. HOIPS I

polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. Also provided are diagnostic methods for detecting abnormal cell proliferation and differentiation disorders and therapeutic methods for treating the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:221411 USPATFULL
TITLE: Human oncogene induced secreted protein I
INVENTOR(S): Olsen, Henrik S., Gaithersburg, MD, UNITED STATES
Ruben, Steven M., Olney, MD, UNITED STATES
PATENT ASSIGNEE(S): Human Genome Sciences, Inc. (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002119552	A1	20020829
APPLICATION INFO.:	US 2001-899917	A1	20010709 (9)
RELATED APPLN. INFO.:	Division of Ser. No. US 1997-994962, filed on 19 Dec 1997, PATENTED		

	NUMBER	DATE
PRIORITY INFORMATION:	US 1996-33869P	19961220 (60)
	US 1997-37388P	19970207 (60)
DOCUMENT TYPE:	Utility	
FILE SEGMENT:	APPLICATION	
LEGAL REPRESENTATIVE:	STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C., 1100 NEW YORK AVENUE, N.W., SUITE 600, WASHINGTON, DC, 20005-3934	
NUMBER OF CLAIMS:	16	
EXEMPLARY CLAIM:	1	
NUMBER OF DRAWINGS:	4 Drawing Page(s)	
LINE COUNT:	2059	

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 2 OF 18 USPATFULL on STN

TI Human oncogene induced secreted protein I
AB The present invention relates to a novel protein, the Human Oncogene Induced Secreted Protein I ("HOIPS I") protein. In particular, isolated nucleic acid molecules are provided encoding the human HOIPS I protein. HOIPS I polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. Also provided are diagnostic methods for detecting abnormal cell proliferation and differentiation disorders and therapeutic methods for treating the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2001:147697 USPATFULL
TITLE: Human oncogene induced secreted protein I
INVENTOR(S): Olsen, Henrik S., Gaithersburg, MD, United States
Ruben, Steven M., Olney, MD, United States
PATENT ASSIGNEE(S): Human Genome Sciences, Inc., Rockville, MD, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6284486	B1	20010904
APPLICATION INFO.:	US 1997-994962		19971219 (8)
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	GRANTED		
PRIMARY EXAMINER:	Carlson, Karen Cochrane		
LEGAL REPRESENTATIVE:	Sterne, Kessler, Goldstein & Fox P.L.L.C.		
NUMBER OF CLAIMS:	69		
EXEMPLARY CLAIM:	1		
NUMBER OF DRAWINGS:	4 Drawing Figure(s); 4 Drawing Page(s)		

LINE COUNT: 1994
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 3 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAW69220 Protein DGENE

AB This sequence is the human oncogene induced secreted protein I (HOIPS I) of the invention. HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAW69220 Protein DGENE

TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p

APPLICATION INFO: WO 1997-US23547 19971219

PRIORITY INFO: US 1997-37388 19970207

US 1996-33869 19961220

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

CROSS REFERENCES: N-PSDB: AAV44745

DESCRIPTION: Human oncogene induced secreted protein I.

L3 ANSWER 4 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44751 cDNA DGENE

AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (HOIPS I). HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44751 cDNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p

APPLICATION INFO: WO 1997-US23547 19971219

PRIORITY INFO: US 1997-37388 19970207

US 1996-33869 19961220

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Expressed sequence tag C02431.

L3 ANSWER 5 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44750 cDNA DGENE
AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (HOIPS I). HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44750 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Expressed sequence tag T84854.

L3 ANSWER 6 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44749 cDNA DGENE
AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (HOIPS I). HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44749 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Expressed sequence tag T92475.

L3 ANSWER 7 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44748 cDNA DGENE
AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (HOIPS I). HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute

and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44748 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Expressed sequence tag T91708.

L3 ANSWER 8 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44758 DNA DGENE
AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (HOIPS I) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44758 DNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 9 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44757 DNA DGENE
AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (HOIPS I) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44757 DNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 10 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44756 DNA DGENE
AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (**HOIPS I**) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44756 DNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 11 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44755 DNA DGENE
AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (**HOIPS I**) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44755 DNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 12 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44754 DNA DGENE

AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (HOIPS I) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44754 DNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p

APPLICATION INFO: WO 1997-US23547 19971219

PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 13 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44753 DNA DGENE

AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (HOIPS I) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44753 DNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p

APPLICATION INFO: WO 1997-US23547 19971219

PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 14 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44752 DNA DGENE

AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (HOIPS I) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44752 DNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used
to develop products for the diagnosis and treatment of cell
proliferative diseases, particularly cancers such as
leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 15 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop
products for the diagnosis and treatment of cell proliferative diseases,
particularly cancers such as leukaemia
AN AAV44746 cDNA DGENE
AB This sequence represents an expressed sequence tag, which is specifically
stated as not being contained within the DNA of the invention. The DNA of
the invention encodes the human oncogene induced secreted protein I (
HOIPS I). HOIPS I can be used for
treating cell proliferative diseases, particularly cancers, such as acute
and chronic myelogenous leukaemias. The products can also be used for
detection and diagnosis of a cell proliferative or cell differentiation
disorders.

ACCESSION NUMBER: AAV44746 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used
to develop products for the diagnosis and treatment of cell
proliferative diseases, particularly cancers such as
leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Expressed sequence tag.

L3 ANSWER 16 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop
products for the diagnosis and treatment of cell proliferative diseases,
particularly cancers such as leukaemia
AN AAV44747 cDNA DGENE
AB This sequence represents an expressed sequence tag, which is specifically
stated as not being contained within the DNA of the invention. The DNA of
the invention encodes the human oncogene induced secreted protein I (
HOIPS I). HOIPS I can be used for
treating cell proliferative diseases, particularly cancers, such as acute
and chronic myelogenous leukaemias. The products can also be used for
detection and diagnosis of a cell proliferative or cell differentiation
disorders.

ACCESSION NUMBER: AAV44747 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used
to develop products for the diagnosis and treatment of cell
proliferative diseases, particularly cancers such as
leukaemia
INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Expressed sequence tag AA340310.

L3 ANSWER 17 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44745 cDNA DGENE
AB This sequence encodes the human oncogene induced secreted protein I (HOIPS I) of the invention. HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44745 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
CROSS REFERENCES: P-PSDB: AAW69220
DESCRIPTION: Human oncogene induced secreted protein I coding sequence.

L3 ANSWER 18 OF 18 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia.
AN 1998-377652 [32] WPIDS
AB WO 9828421 A UPAB: 19980812
An isolated nucleic acid molecule (I) is claimed comprising a polynucleotide (PN) having a nucleotide sequence (NS) at least 95% identical to a sequence selected from:
(a) a NS encoding a polypeptide comprising amino acids from -20 to 142, -19 to 142, or 1 to 142 of the 162 amino acid (aa) sequence given in the specification (sequence representing a Human Oncogene Induced Secreted Protein I (HOIPS I) polypeptide);
(b) a NS encoding a polypeptide having an amino acid sequence encoded by a cDNA clone contained in ATCC 97825;
(c) a NS encoding a mature HOIPS I polypeptide having an amino acid sequence encoded by a cDNA clone contained in ATCC 97825; and
(d) a NS complementary to any of the NSs in (a)-(c).
Also claimed are:
(1) an isolated Nucleic Acid Molecule (NAM) comprising a PN which hybridises under stringent hybridisation conditions (I) where the PN which hybridises does not hybridise under stringent hybridisation conditions to a PN having a NS consisting of only A residues or of only T residues;
(2) an isolated NAM comprising a PN which encodes an amino acid sequence of an epitope-bearing portion of a HOIPS I

polypeptide having an amino acid sequence as in (a)-(c) above;

(3) an isolated NAM comprising a PN having a sequence at least 95% identical to a sequence selected from:

(a) a NS of a fragment of a 860 bp sequence given in the specification (encoding the HOIPS I polypeptide), where the fragment comprises at least 50 contiguous nucleotides of the 860 bp, provided that the NS is not one of the 514, 457, 413, 320, 264, and 249 sequences given in the specification; and

(b) a NS complementary to a NS as in (a);

(4) a method for making a recombinant vector comprising inserting (I) into a vector;

(5) a recombinant vector produced by a method as in (4);

(6) a method of making a recombinant host cell comprising introducing a recombinant vector as in (5) into a host cell;

(7) a recombinant host cell produced by a method as in (6);

(8) an isolated HOIPS I polypeptide having an amino acid sequence at least 95% identical to a sequence encoded by (I) or an epitope-bearing portion of the polypeptide;

(9) an isolated polypeptide comprising an epitope-bearing portion of the HOIPS I protein, where the portion is selected from a polypeptide comprising amino acid residues from -4 to 9, from 13 to 19, from 23 to 32, from 36 to 47, from 54 to 63, from 70 to 74, from 90 to 100, from 105 to 119 or from 125 to 132 of the 162 aa sequence;

(10) an isolated HOIPS I polypeptide where, except for 1 to 50 conservative amino acid substitutions, the polypeptide has a sequence selected from:

(a) amino acids from -20 to 142, 19 to 142, or 1 to 142 of the 162 aa sequence given in the specification;

(b) an amino acid sequence of the HOIPS I polypeptide having an amino acid sequence encoded by a cDNA contained in ATCC 97825;

(c) an amino acid sequence of a mature HOIPS I polypeptide having an amino acid sequence encoded by a cDNA clone contained in ATCC 97825; and

(d) an amino acid sequence of an epitope-bearing portion of any one of the polypeptides as in (a)-(c);

(11) an isolated nucleic acid encoding a polypeptide as in (10).

USE - The products can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis.

Dwg.0/3

ACCESSION NUMBER: 1998-377652 [32] WPIDS
DOC. NO. NON-CPI: N1998-295209
DOC. NO. CPI: C1998-114764
TITLE: New isolated human oncogene induced secreted protein -
used to develop products for the diagnosis and treatment
of cell proliferative diseases, particularly cancers such
as leukaemia.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): OLSEN, H S; RUBEN, S M
PATENT ASSIGNEE(S): (HUMA-N) HUMAN GENOME SCI INC
COUNTRY COUNT: 81
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9828421	A1	19980702	(199832)*	EN	71
RW: AT BE CH DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA					
PT SD SE SZ UG ZW					
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE					
GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG					
MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG					
US UZ VN YU ZW					
AU 9858027	A	19980717	(199848)		

APPLICATION DETAILS:

FILING DETAILS:

PRIORITY APPLN. INFO: US 1997-37388P 19970207; US
1996-33869P 19961220; US
1997-994962 19971219; US
2001-899917 20010709

Refine Search

Search Results -

Terms	Documents
L9 and L10	18

Database:

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 US Patents Full-Text Database
 US OCR Full-Text Database
 EPO Abstracts Database
 JPO Abstracts Database
 Derwent World Patents Index
 IBM Technical Disclosure Bulletins

Search:

L11

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DATE: Thursday, April 29, 2004 [Printable Copy](#) [Create Case](#)

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result set

DB=USPT; PLUR=YES; OP=OR

<u>L11</u>	19 and L10	18	<u>L11</u>
<u>L10</u>	ruben.in.	1520	<u>L10</u>
<u>L9</u>	l6 and L8	31	<u>L9</u>
<u>L8</u>	olsen.in.	2539	<u>L8</u>
<u>L7</u>	henrik-olsen.in.	0	<u>L7</u>
<u>L6</u>	myelogenous leukemia and L5	10350	<u>L6</u>
<u>L5</u>	myeloid proliferation and l4	29144	<u>L5</u>
<u>L4</u>	L3 and protein sequence	614907	<u>L4</u>
<u>L3</u>	human oncogene induced secreted protein I	1403401	<u>L3</u>
<u>L2</u>	HOIPs-I	0	<u>L2</u>
<u>L1</u>	6284486.pn.	1	<u>L1</u>

END OF SEARCH HISTORY

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Search Results - Record(s) 1 through 10 of 18 returned.

☐ 1. Document ID: US 6632920 B1

L11: Entry 1 of 18

File: USPT

Oct 14, 2003

US-PAT-NO: 6632920

DOCUMENT-IDENTIFIER: US 6632920 B1

TITLE: 36 human secreted proteins

DATE-ISSUED: October 14, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Olsen</u> ; Henrik S.	Gaithersburg	MD		
<u>Ruben</u> ; Steven M.	Olney	MD		
Rosen; Craig A.	Laytonsville	MD		
Brewer; Laurie A.	St. Paul	MN		
Ebner; Reinhard	Gaithersburg	MD		
Duan; Roxanne	Bethesda	MD		
Florence; Kimberly	Rockville	MD		

US-CL-CURRENT: 530/300; 435/69.1, 530/324

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sanctions	Attachments	Claims	KWIC	Drawings
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☐ 2. Document ID: US 6627741 B2

L11: Entry 2 of 18

File: USPT

Sep 30, 2003

US-PAT-NO: 6627741

DOCUMENT-IDENTIFIER: US 6627741 B2

TITLE: Antibodies to secreted protein HCEJQ69

DATE-ISSUED: September 30, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Ruben</u> ; Steven M.	Olney	MD		
Ni; Jian	Germantown	MD		

h e b b g e e f e ef b e

Rosen; Craig A.	Laytonsville	MD
Wei; Ying-Fei	Berkeley	CA
Young; Paul	Gaithersburg	MD
Florence; Kimberly	Rockville	MD
Soppet; Daniel R.	Centreville	VA
Brewer; Laurie A.	St. Paul	MN
Endress; Gregory A.	Florence	MA
Carter; Kenneth C.	North Potomac	MD
Mucenski; Michael	Cincinnati	OH
Ebner; Reinhard	Gaithersburg	MD
LaFleur; David W.	Washington	DC
<u>Olsen</u> ; Henrik	Gaithersburg	MD
Shi; Yanggu	Gaithersburg	MD
Moore; Paul A.	Germantown	MD
Komatsoulis; George	Silver Spring	MD

US-CL-CURRENT: 530/389.2; 530/387.1, 530/387.3, 530/387.7, 530/387.9, 530/388.1,
530/388.15, 530/389.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Drawings	Claims	KMC	Draw Data
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☐ 3. Document ID: US 6605592 B2

L11: Entry 3 of 18

File: USPT

Aug 12, 2003

US-PAT-NO: 6605592

DOCUMENT-IDENTIFIER: US 6605592 B2

TITLE: Protein HOFNF53

DATE-ISSUED: August 12, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ni; Jian	Germantown	MD		
Baker; Kevin P.	Darnestown	MD		
Birse; Charles E.	North Potomac	MD		
Ebner; Reinhard	Gaithersburg	MD		
Fiscella; Michele	Bethesda	MD		
Komatsoulis; George A.	Silver Spring	MD		
LaFleur; David W.	Washington	DC		
Moore; Paul A.	Germantown	MD		
<u>Olsen</u> ; Henrik S.	Gaithersburg	MD		
Rosen; Craig A.	Laytonsville	MD		
<u>Ruben</u> ; Steven M.	Olney	MD		
Soppet; Daniel R.	Centreville	VA		
Young; Paul E.	Gaithersburg	MD		
Wei; Ping	Brookeville	MD		

h e b b g e e e f e ef b e

Florence; Kimberly A. Rockville MD

US-CL-CURRENT: 514/2, 435/252.3, 435/254.11, 435/320.1, 435/325, 435/471, 435/69.1,
435/71.1, 435/71.2, 514/12, 514/8, 530/350

Full	Title	Citation	Front	Review	Classification	Date	Reference	Examiner's	Attachments	Claims	KWMC	Drawings
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☐ 4. Document ID: US 6590075 B2

L11: Entry 4 of 18

File: USPT

Jul 8, 2003

US-PAT-NO: 6590075

DOCUMENT-IDENTIFIER: US 6590075 B2

TITLE: Secreted protein HODAZ50

DATE-ISSUED: July 8, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Ruben</u> ; Steven M.	Olney	MD		
Rosen; Craig A.	Laytonsville	MD		
Fischer; Carrie L.	Burke	VA		
Soppet; Daniel R.	Centreville	VA		
Carter; Kenneth C.	North Potomac	MD		
Bednarik; Daniel P.	Columbia	MD		
Endress; Gregory A.	Potomac	MD		
Yu; Guo-Liang	Berkeley	CA		
Ni; Jian	Rockville	MD		
Feng; Ping	Gaithersburg	MD		
Young; Paul E.	Gaithersburg	MD		
Greene; John M.	Gaithersburg	MD		
Ferrie; Ann M.	Tewksbury	MA		
Duan; Roxanne	Bethesda	MD		
Hu; Jing-Shan	Sunnyvale	CA		
Florence; Kimberly A.	Rockville	MD		
<u>Olsen</u> ; Henrik S.	Gaithersburg	MD		
Ebner; Reinhard	Gaithersburg	MD		
Brewer; Laurie A.	St. Paul	MN		
Shi; Yanggu	Gaithersburg	MD		

US-CL-CURRENT: 530/350; 435/6, 435/69.1, 435/7.1, 536/23.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Examiner's	Attachments	Claims	KWMC	Drawings
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☐ 5. Document ID: US 6576445 B1

L11: Entry 5 of 18

File: USPT

Jun 10, 2003

US-PAT-NO: 6576445
DOCUMENT-IDENTIFIER: US 6576445 B1

TITLE: Chemokine .alpha.-4

DATE-ISSUED: June 10, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Olsen</u> ; Henrik S.	Gaithersburg	MD		
<u>Ruben</u> ; Steven M.	Olney	MD		
Zeng; Zhi-Zhen	Gaithersburg	MD		

US-CL-CURRENT: 435/69.5; 435/325, 530/300, 530/350, 530/386, 530/387.1, 530/387.3,
530/387.9, 530/388.1, 530/388.15, 530/388.23, 530/389.1, 530/389.2, 530/391.1,
530/391.3, 530/391.5, 530/391.7, 530/391.9

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KIMC	Draw De
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☐ 6. Document ID: US 6566325 B2

L11: Entry 6 of 18

File: USPT

May 20, 2003

US-PAT-NO: 6566325
DOCUMENT-IDENTIFIER: US 6566325 B2

TITLE: 49 human secreted proteins

DATE-ISSUED: May 20, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Moore; Paul A.	Germantown	MD		
<u>Ruben</u> ; Steven M.	Olney	MD		
<u>Olsen</u> ; Henrik S.	Gaithersburg	MD		
Shi; Yanggu	Gaithersburg	MD		
Rosen; Craig A.	Laytonsville	MD		
Florence; Kimberly A.	Rockville	MD		
Soppet; Daniel R.	Centreville	VA		
LaFleur; David W.	Washington	DC		
Endress; Gregory A.	Potomac	MD		
Ebner; Reinhard	Gaithersburg	MD		
Komatsoulis; George	Silver Spring	MD		
Duan; Roxanne D.	Bethesda	MD		

US-CL-CURRENT: 514/2; 530/300, 530/350

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KIMC	Draw De
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☐ 7. Document ID: US 6548063 B1

L11: Entry 7 of 18

File: USPT

Apr 15, 2003

US-PAT-NO: 6548063

DOCUMENT-IDENTIFIER: US 6548063 B1

TITLE: Synferon

DATE-ISSUED: April 15, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Olsen</u> ; Henrik S.	Gaithersburg	MD		
Gentz; Reiner L.	Rockville	MD		
<u>Ruben</u> ; Steven M.	Olney	MD		

US-CL-CURRENT: 424/158.1; 424/85.4, 435/325, 530/350, 530/351, 530/388.1, 530/389.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Examiner's	Alterations	Claims	KWMC	Draw. D.
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☐ 8. Document ID: US 6534631 B1

L11: Entry 8 of 18

File: USPT

Mar 18, 2003

US-PAT-NO: 6534631

DOCUMENT-IDENTIFIER: US 6534631 B1

TITLE: Secreted protein HT5GJ57

DATE-ISSUED: March 18, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Ruben</u> ; Steven M.	Olney	MD		
Komatsoulis; George	Silver Spring	MD		
Duan; Roxanne D.	Bethesda	MD		
Rosen; Craig A.	Laytonsville	MD		
Moore; Paul A.	Germantown	MD		
Shi; Yanggu	Gaithersburg	MD		
LaFleur; David W.	Washington	DC		
Ebner; Reinhard	Gaithersburg	MD		
<u>Olsen</u> ; Henrik	Gaithersburg	MD		
Brewer; Laurie A.	St. Paul	MN		
Florence; Kimberly A.	Rockville	MD		
Young; Paul	Gaithersburg	MD		
Mucenski; Michael	Cincinnati	OH		
Endress; Gregory A.	Potomac	MD		
Soppet; Daniel R.	Centreville	VA		

US-CL-CURRENT: 530/350; 435/320.1, 435/325, 530/300, 536/23.1, 536/24.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Drawings
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☐ 9. Document ID: US 6525174 B1

L11: Entry 9 of 18

File: USPT

Feb 25, 2003

US-PAT-NO: 6525174

DOCUMENT-IDENTIFIER: US 6525174 B1

TITLE: Precerebellin-like protein

DATE-ISSUED: February 25, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Young; Paul	Gaithersburg	MD		
Greene; John M.	Gaithersburg	MD		
Ferrie; Ann M.	Tewksbury	MA		
<u>Ruben</u> ; Steven M.	Olney	MD		
Rosen; Craig A.	Laytonsville	MD		
Hu; Jing-Shan	Sunnyvale	CA		
<u>Olsen</u> ; Henrik S.	Gaithersburg	MD		
Ebner; Reinhard	Gaithersburg	MD		
Brewer; Laurie A.	St. Paul	MN		
Moore; Paul A.	Germantown	MD		
Shi; Yanggu	Gaithersburg	MD		
Florence; Charles	Rockville	MD		
Florence; Kimberly	Rockville	MD		
Lafleur; David W.	Washington	DC		
Ni; Jian	Rockville	MD		
Fan; Ping	Gaithersburg	MD		
Wei; Ying-Fei	Berkeley	CA		
Fischer; Carrie L.	Burke	VA		
Soppet; Daniel R.	Centreville	VA		
Li; Yi	Sunnyvale	CA		
Zeng; Zhizhen	Gaithersburg	MD		
Kyaw; Hla	Frederick	MD		
Yu; Guo-Liang	Berkeley	CA		
Feng; Ping	Gaithersburg	MD		
Dillon; Patrick J.	Carlsbad	CA		
Endress; Gregory A.	Potomac	MD		
Carter; Kenneth C.	North Potomac	MD		

US-CL-CURRENT: 530/350; 435/69.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Drawings
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☐ 10. Document ID: US 6476195 B1

L11: Entry 10 of 18

File: USPT

Nov 5, 2002

US-PAT-NO: 6476195

DOCUMENT-IDENTIFIER: US 6476195 B1

TITLE: Secreted protein HNFGF20

DATE-ISSUED: November 5, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Komatsoulis; George	Silver Spring	MD		
Rosen; Craig A.	Laytonsville	MD		
<u>Ruben</u> ; Steven M.	Olney	MD		
Duan; Roxanne D.	Bethesda	MD		
Moore; Paul A.	Germantown	MD		
Shi; Yanggu	Gaithersburg	MD		
LaFleur; David W.	Washington	DC		
Wei; Ying-Fei	Berkeley	CA		
Ni; Jian	Rockville	MD		
Florence; Kimberly A.	Rockville	MD		
Young; Paul	Gaithersburg	MD		
Brewer; Laurie A.	St. Paul	MN		
Soppet; Daniel R.	Centreville	VA		
Endress; Gregory A.	Potomac	MD		
Ebner; Reinhard	Gaithersburg	MD		
<u>Olsen</u> ; Henrik	Gaithersburg	MD		
Mucenski; Michael	Cincinnati	OH		

US-CL-CURRENT: 530/350; 435/6, 435/7.1, 536/23.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KOMIC	Draw D
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Terms	Documents
L9 and L10	18

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☐ 11. Document ID: US 6475753 B1

L11: Entry 11 of 18

File: USPT

Nov 5, 2002

US-PAT-NO: 6475753

DOCUMENT-IDENTIFIER: US 6475753 B1

TITLE: 94 Human Secreted Proteins

DATE-ISSUED: November 5, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Ruben</u> ; Steven M.	Olney	MD		
Ni; Jian	Rockville	MD		
Rosen; Craig A.	Laytonsville	MD		
Wei; Ying-Fei	Berkeley	CA		
Young; Paul	Gaithersburg	MD		
Florence; Kimberly	Rockville	MD		
Soppet; Daniel R.	Centreville	VA		
Brewer; Laurie A.	St. Paul	MN		
Endress; Gregory A.	Potomac	MD		
Carter; Kenneth C.	Potomac	MD		
Mucenski; Michael	Cincinnati	OH		
Ebner; Reinhard	Gaithersburg	MD		
Lafleur; David W.	Washington	DC		
<u>Olsen</u> ; Henrik	Gaithersburg	MD		
Shi; Yanggu	Gaithersburg	MD		
Moore; Paul A.	Germantown	MD		
Komatsoulis; George	Silver Spring	MD		

US-CL-CURRENT: 435/69.1; 435/252.3, 435/320.1, 435/325, 435/471, 435/69.4,
435/71.1, 530/350, 536/23.5

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draws	Doc
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☐ 12. Document ID: US 6433139 B1

L11: Entry 12 of 18

File: USPT

Aug 13, 2002

US-PAT-NO: 6433139
DOCUMENT-IDENTIFIER: US 6433139 B1

TITLE: Secreted protein HPEAD48

DATE-ISSUED: August 13, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Ruben</u> ; Steven M.	Olney	MD		
Rosen; Craig A.	Laytonsville	MD		
<u>Olsen</u> ; Henrik S.	Gaithersburg	MD		

US-CL-CURRENT: 530/350; 435/6, 435/7.1, 530/300, 536/23.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequence	Attachment	Claims	KIMC	Draw D
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☐ 13. Document ID: US 6420526 B1

L11: Entry 13 of 18

File: USPT

Jul 16, 2002

US-PAT-NO: 6420526
DOCUMENT-IDENTIFIER: US 6420526 B1

TITLE: 186 human secreted proteins

DATE-ISSUED: July 16, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Ruben</u> ; Steven M.	Olney	MD		
Rosen; Craig A.	Laytonsville	MD		
Fischer; Carrie L.	Burke	VA		
Soppet; Daniel P.	Centreville	VA		
Carter; Kenneth C.	North Potomac	MD		
Bednarik; Daniel R.	Columbia	MD		
Endress; Gregory A.	Potomac	MD		
Yu; Guo-Liang	Berkeley	CA		
Ni; Jian	Rockville	MD		
Feng; Ping	Gaithersburg	MD		
Young; Paul E.	Gaithersburg	MD		
Greene; John M.	Gaithersburg	MD		
Ferrie; Ann M.	Tewksbury	MA		
Duan; Roxanne	Bethesda	MD		
Hu; Jing-Shan	Sunnyvale	CA		
Florence; Kimberly A.	Rockville	MD		
<u>Olsen</u> ; Henrik S.	Gaithersburg	MD		
Ebner; Reinhard	Gaithersburg	MD		
Brewer; Laurie A.	St. Paul	MN		

Moore; Paul A.	Germantown	MD
Shi; Yanggu	Gaithersburg	MD
Lafleur; David W.	Washington	DC
Li; Yi	Sunnyvale	CA
Zeng; Zhizhen	Lansdale	PA
Kyaw; Hla	Frederick	MD

US-CL-CURRENT: 530/350; 435/6, 536/23.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequence	Abstracts	Claims	KWIC	Draw. De
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☐ 14. Document ID: US 6379926 B1

L11: Entry 14 of 18

File: USPT

Apr 30, 2002

US-PAT-NO: 6379926

DOCUMENT-IDENTIFIER: US 6379926 B1

TITLE: Polynucleotides encoding chemokine .beta.-6 antagonists

DATE-ISSUED: April 30, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Kreider; Brent L.	Germantown	MD		
Ruben; Steven M.	Olney	MD		
Olsen; Henrik S.	Gaithersburg	MD		

US-CL-CURRENT: 435/69.5; 435/252.3, 435/320.1, 435/325, 435/455, 435/471, 435/69.1,
435/69.7, 536/23.1, 536/23.4, 536/23.5

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequence	Abstracts	Claims	KWIC	Draw. De
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☐ 15. Document ID: US 6342581 B1

L11: Entry 15 of 18

File: USPT

Jan 29, 2002

US-PAT-NO: 6342581

DOCUMENT-IDENTIFIER: US 6342581 B1

**** See image for Certificate of Correction ****TITLE: Secreted protein HLHFP03

DATE-ISSUED: January 29, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Rosen; Craig A.	Laytonsville	MD		
Ruben; Steven M.	Olney	MD		

Olsen; Henrik S. Gaithersburg MD
Ebner; Reinhard Gaithersburg MD

US-CL-CURRENT: 530/300; 435/69.1, 530/350

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMCC	Draw De
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☐ 16. Document ID: US 6284486 B1

L11: Entry 16 of 18

File: USPT

Sep 4, 2001

US-PAT-NO: 6284486

DOCUMENT-IDENTIFIER: US 6284486 B1

TITLE: Human oncogene induced secreted protein I

DATE-ISSUED: September 4, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Olsen</u> ; Henrik S.	Gaithersburg	MD		
<u>Ruben</u> ; Steven M.	Olney	MD		

US-CL-CURRENT: 435/69.1; 435/252.3, 435/6, 435/91.1, 435/91.4, 435/91.41, 536/23.1,
536/23.5, 536/24.1, 536/24.2

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMCC	Draw De
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☐ 17. Document ID: US 6114145 A

L11: Entry 17 of 18

File: USPT

Sep 5, 2000

US-PAT-NO: 6114145

DOCUMENT-IDENTIFIER: US 6114145 A

TITLE: Synferon, a synthetic interferon

DATE-ISSUED: September 5, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Olsen</u> ; Henrik S.	Gaithersburg	MD		
Gentz; Reiner L.	Rockville	MD		
<u>Ruben</u> ; Steven M.	Olney	MD		

US-CL-CURRENT: 435/69.51; 424/85.4, 435/252.3, 435/252.33, 435/254.11, 435/325,
435/455, 435/471, 435/91.41, 530/351, 536/23.52

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMCC	Draw De
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☐ 18. Document ID: US 5916769 A

L11: Entry 18 of 18

File: USPT

Jun 29, 1999

US-PAT-NO: 5916769

DOCUMENT-IDENTIFIER: US 5916769 A

TITLE: Polynucleotides encoding extra cellular/epidermal growth factor HCABA58X polypeptides

DATE-ISSUED: June 29, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Olsen</u> ; Henrik S.	Gaithersburg	MD		
<u>Ruben</u> ; Steven M.	Olney	MD		

US-CL-CURRENT: 435/69.4; 435/243, 435/320.1, 435/325, 435/69.1, 536/23.1, 536/23.51

Full	Title	Citation	Front	Review	Classification	Date	Reference	Continuation	Related	Claims	KIMC	Draw Data
------	-------	----------	-------	--------	----------------	------	-----------	--------------	---------	--------	------	-----------

Clear	Generate Collection	Print	Fwd Refs	Bkwd Refs	Generate OACS
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Terms	Documents
L9 and L10	18

Display Format: [Previous Page](#)[Next Page](#)[Go to Doc#](#)

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OM protein - protein search, using sw model

Run on: April 29, 2004, 15:21:06 ; Search time 58 Seconds

(without alignments)
789.184 Million cell updates/sec

Title: US-09-899-917-2

Sequence score: 1 MGFMRTPLMTLIPFSCSG.....ELYTEKSTVACANATIMCS 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	862	100.0	162	2	AAW69220 Human onc
2	862	100.0	162	2	AAW69220 Human onc
3	862	100.0	162	2	AAW69220 Human onc
4	854	99.1	162	3	AAW77476 Human pro
5	850	98.6	162	6	ABU61841 Human MD1
6	758	87.9	162	3	AAW64000 Human B-c
7	613	71.1	162	2	AAW69220 Human onc
8	613	71.1	162	3	AAW77481 Rodent pr
9	613	71.1	162	3	ABU61846 Mouse MD1
10	613	71.1	162	7	ADBS9272 Rat Prote
11	336	39.0	160	3	AAW77482 Avian pro
12	336	39.0	160	6	ABU61847 Chicken M
13	106	12.3	160	2	AAW69220 Human onc
14	106	12.3	160	3	AAW69220 Human onc
15	101.5	11.8	160	2	AAW69220 Human onc
16	101.5	11.8	160	3	AAW69220 Human onc
17	101.5	11.8	160	3	AAW69220 Human onc
18	101.5	11.8	160	6	ABU61843 Human MD-
19	96.5	11.2	141	3	AAW77480 Updated h
20	96.5	11.2	141	6	ABU61845 Mouse MD2
21	79.5	9.2	141	6	ABU61845 Mouse MD2
22	78	9.0	876	6	ABU6402 Protein e
23	77	8.9	363	3	AAW69220 Human onc
24	77	8.9	364	3	AAW69220 Human onc
25	76.5	8.9	1177	6	ABU17986 Protein e

26	75.5	8.8	342	6	ABU26566 Protein e
27	75.5	8.8	1200	3	AAW69220 Human onc
28	75.5	8.8	1207	3	AAW69220 Human onc
29	75.5	8.8	1215	3	AAW69220 Human onc
30	75.5	8.8	1241	6	ABU24033 Protein e
31	75.5	8.7	377	2	AAW69220 Human onc
32	75.5	8.7	505	7	ADBS75603 Prostate
33	75.5	8.7	505	7	ADBS75603 Prostate
34	75.5	8.7	524	3	AAW69220 Human onc
35	75.5	8.7	699	5	ABW91291 Herbicida
36	74	8.6	392	2	AAW69220 Human onc
37	73.5	8.5	264	2	AAW69220 Human onc
38	72.5	8.4	851	7	ADBS6435 KIRA1196
39	72.5	8.4	1172	5	ABP63009 Human pol
40	72.5	8.4	1178	5	ABP63008 Human pol
41	72	8.4	269	4	ABW95041 Human pro
42	72	8.4	608	5	ABP65007 Human pro
43	72	8.4	700	5	ABW92360 Herbicida
44	72	8.4	790	5	AAW69220 Human onc
45	71.5	8.3	310	6	ABW70549 Phototrab

ALIGNMENTS

RESULT 1

ID AAW69220 standard; protein, 162 AA.

16-OCT-1998 (first entry)

Human oncogene induced secreted protein I.

Oncogene induced secreted protein I; HOIPS I; human; cancer; therapy;

cell proliferative disease; myelogenous leukaemia;

cell differentiation disorder.

Homo sapiens.

Key Location/Qualifiers

Peptide /note= "signal peptide"

Protein /note= "mature HOIPS I"

WO9828421-A1.

02-JUL-1998.

19-DEC-1997; 97WO-US023547.

20-DEC-1996; 96US-0033869P.

07-FEB-1997; 97US-0037388P.

(HUMA-) HUMAN GENOME SCI INC.

Olsen HS, Ruben SM;

WPI, 1998-377652/32.

N-PSDB; AAV44745.

New isolated human oncogene induced secreted protein - used to develop

products for the diagnosis and treatment of cell proliferative diseases,

particularly cancers such as leukaemia.

Claim 12; Page 51-52; 71pp; English.

This sequence is the human oncogene induced secreted protein I (HOIPS I)

of the invention. HOIPS I can be used for treating cell proliferative

diseases, particularly cancers, such as acute and chronic myelogenous

leukaemias. The products can also be used for detection and diagnosis of

CC a cell proliferative or cell differentiation disorders
XX
SQ Sequence 162 AA;
Query Match 100.0%; Score 862; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 9e-92;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MKGFTATLFLMTLIFPSCSGGGGKAMPHTVVCSDSGLEVLVYQSCDPLQDFGFSVEKCSK 60
DB 1 MKGFTATLFLMTLIFPSCSGGGGKAMPHTVVCSDSGLEVLVYQSCDPLQDFGFSVEKCSK 60
OY 61 QLKSNINIRFGIILREDIKELFLDLALMSQSSVYNFSYPICEALPFFSFCGRKGEQI 120
DB 61 QLKSNINIRFGIILREDIKELFLDLALMSQSSVYNFSYPICEALPFFSFCGRKGEQI 120
OY 121 YYAGPVNNEFTTPOGEYQVLELTYEKRSITVACANATIMCS 162
DB 121 YYAGPVNNEFTTPOGEYQVLELTYEKRSITVACANATIMCS 162
RESULT 2
AA13933
ID AA13933 standard; protein; 162 AA.
XX
AC AA13933;
XX
DT 14-JUN-1999 (first entry)
XX
DE Human OHP106 protein.
XX
KM OHP106; bacterial; viral; infection; cytokine activity; tissue formation;
KM cell proliferation; cell differentiation; immunostimulation; therapy;
KM immunosuppression; haematopoiesis control; tissue repair.
XX
OS Homo sapiens.
XX
PN MO9918205-A1.
XX
PD 15-APR-1999.
XX
PF 06-OCT-1998; 98WO-JP004515.
XX
PR 07-OCT-1997; 97JP-00274673.
XX
PA (ONCOY) ONO PHARM CO LTD.
XX
PI Honjo T, Kato K, Tada H;
XX
DR WPI; 1999-277269/23.
DR N-PSDB; AAX36695; AAX36696.
XX
PT New polypeptides useful in the treatment of various diseases including
PT bacterial and viral infections with cytokine activity.
XX
PS Claim 1; Page 47; 57pp; Japanese.
XX
CC This sequence represents a OHP106 protein of the invention. The
CC polypeptides and their antibodies are applicable in drug compositions,
CC useful for treatment of various diseases including bacterial and viral
CC infections with cytokine activity, and activities e.g. on cell
CC proliferation/differentiation, immunostimulation/suppression, control of
CC haematopoiesis, and tissue formation and repair. The proteins and
CC antibodies have a wide spectrum of activities
SQ Sequence 162 AA;
Query Match 100.0%; Score 862; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 9e-92;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MKGFTATLFLMTLIFPSCSGGGGKAMPHTVVCSDSGLEVLVYQSCDPLQDFGFSVEKCSK 60
XX

DB 1 MKGFTATLFLMTLIFPSCSGGGGKAMPHTVVCSDSGLEVLVYQSCDPLQDFGFSVEKCSK 60
OY 61 QLKSNINIRFGIILREDIKELFLDLALMSQSSVYNFSYPICEALPFFSFCGRKGEQI 120
DB 61 QLKSNINIRFGIILREDIKELFLDLALMSQSSVYNFSYPICEALPFFSFCGRKGEQI 120
OY 121 YYAGPVNNEFTTPOGEYQVLELTYEKRSITVACANATIMCS 162
DB 121 YYAGPVNNEFTTPOGEYQVLELTYEKRSITVACANATIMCS 162
RESULT 3
ADE59274
ID ADE59274 standard; protein; 162 AA.
XX
AC ADE59274;
XX
DT 29-JUN-2004 (first entry)
XX
DE Human Protein O95711, SEQ ID NO 5168.
XX
KM Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
KM spared nerve injury; SNr; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (PARB) BAYER AG.
XX
PI Woolf C, D'Urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; O95711.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNr)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 162 AA;

Query Match 100.0%; Score 862; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 9e-92;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKGFTATLFWTLTLPSCGGGGRKAMPYVVCSDGLEVLVYQSCDPLQDPFGSVKCKSK 60
 DB 1 MKGFTATLFWTLTLPSCGGGGRKAMPYVVCSDGLEVLVYQSCDPLQDPFGSVKCKSK 60
 QY 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVLPFSPICEALPKFSGRRKGEQI 120
 DB 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVLPFSPICEALPKFSGRRKGEQI 120
 QY 121 YYAGPVNNPEFTIPQGEYQVLLLELYTEKSTVACANATIMCS 162
 DB 121 YYAGPVNNPEFTIPQGEYQVLLLELYTEKSTVACANATIMCS 162

RESULT 4
 AA77476
 ID AA77476 standard; protein; 162 AA.

XX AA77476;
 AC AA77476;
 XX
 DT 05-JUN-2000 (first entry)
 XX

DE Human MD-1 protein.

KW MD-1; MD-2; leucine-rich motif; LRR protein ligand; immune disorder;
 KM inflammation; allergy; immunosuppressant; anaphylactic; anti-rheumatoid;
 XX anti-inflammatory; dermatological; antithyroid.

OS Homo sapiens.

PN WO200001817-A2.

PD 13-JAN-2000.

XX 06-JUL-1999; 99WO-US012366.

XX 06-JUL-1999; 98US-00110938.

XX 13-JUL-1998; 98US-00114466.

XX 23-JUL-1998; 98US-0093897P.

XX 12-AUG-1998; 98US-00132968.

XX 18-AUG-1998; 98US-00136214.

XX 11-SEP-1998; 98US-0099999P.

XX (SCHE) SCHERING CORP.

XX Bates EM, Lebecque SE, Murphy EE, Mattson JD, Gorman DM,
 PI Fedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA;
 PI Bazan JF, Mahony D, Lees EM;
 XX
 XX WPI; 2000-171015/15.
 DR N-PSDB; AA292417.

XX New isolated mammalian genes, used to develop products for treating e.g.
 PT immune, inflammatory or allergic abnormalities, cancers or degenerative
 PT conditions.

XX Claim 43; Page 203-204; 218pp; English.

XX The invention relates to a number of primate and/or rodent proteins, and
 CC the genes which encode them. The invention encompasses human dendritic
 CC cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis factor)
 CC receptor family-related proteins HD1EAB4, HSLJD37R and RANKL; human CC
 CC chemokine HCC5; human dendritic proteins Dub11 and Dub 12; human
 PI

CC MD-1 and human and murine MD-2 proteins, which exhibit the properties of
 CC ligands for proteins comprising a leucine-rich motif (LRR); human cyclin
 CC E2; cDNAs encoding these proteins; and antibodies against these proteins.
 CC The proteins can be used for modulating the physiology or development of
 CC a cell. They can be used to mediate uptake of substrates (e.g.,
 CC prostaglandin-like molecules), to modulate or mediate cellular
 CC interactions (e.g., induce or prevent trafficking, proliferation, or
 CC differentiation of cells), or are intracellular proteins which are
 CC important in various cellular processes such as the dendritic maturation of
 CC proteins or cell cycle regulation. The products can be used for treating
 CC medical conditions such as immune, inflammatory or allergic disorders, or
 CC abnormal cellular proliferation, for example, cancers or degenerative
 CC conditions. They can be used to modulate immune responses in disease
 CC states e.g., autoimmune disorders, including rheumatoid arthritis,
 CC systemic lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well
 CC as acute and chronic inflammatory responses in which T cell activation,
 CC expansion, and/or immunological T cell memory play an important role.
 CC Sequences AA77476-Y77480 represent MD-1 and MD-2 proteins. AA77476 is
 CC human MD-1, AA77477-Y77478 are human MD-2 proteins, AA77479 is murine
 CC MD-2 and AA77480 is a primate MD-2

XX Sequence 162 AA;

Query Match 99.1%; Score 854; DB 3; Length 162;
 Best Local Similarity 99.4%; Pred. No. 7.7e-91;
 Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKGFTATLFWTLTLPSCGGGGRKAMPYVVCSDGLEVLVYQSCDPLQDPFGSVKCKSK 60
 DB 1 MKGFTATLFWTLTLPSCGGGGRKAMPYVVCSDGLEVLVYQSCDPLQDPFGSVKCKSK 60
 QY 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVLPFSPICEALPKFSGRRKGEQI 120
 DB 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVLPFSPICEALPKFSGRRKGEQI 120
 QY 121 YYAGPVNNPEFTIPQGEYQVLLLELYTEKSTVACANATIMCS 162
 DB 121 YYAGPVNNPEFTIPQGEYQVLLLELYTEKSTVACANATIMCS 162

RESULT 5
 AB061841
 ID AB061841 standard; protein; 162 AA.

XX AB061841;

XX 15-AUG-2003 (first entry)

XX Human MD1.

XX Human; MD1; cell development; tissue culture development.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT Misc-difference 13 /label= Unknown

XX FT Misc-difference 37 /note= "Encoded by CTM"

XX FT Misc-difference 37 /label= Unknown

XX FT /note= "Encoded by SKY"

XX US2003028005-A1.

XX 06-FEB-2003.

XX 11-AUG-1999; 99US-00372348.

XX 12-AUG-1998; 98US-0096328P.

XX (BAZA) BAZAN J F.
 XX Bazan JF;
 PI

XX WPI: 2003-466159/44.
DR N-PSDB; AKA62461.
XX
XX New composition comprising HCC5, Dab11, Dab12, primate MD1 or MD2 or
PT rodent MD2 polypeptide, useful for modulating physiology or development
XX of a cell or tissue culture cells.
XX
PS Claim 1; Page 15-16; 77p; English.
XX
CC The invention relates to a novel chemokine, de-ubiquitination or cell
CC surface protein. The composition is useful for modulating physiology or
CC development of a cell or tissue culture cells. The present sequence
CC represents the amino acid sequence of human MD1
XX
SQ Sequence 162 AA;
Query Match 98.6%; Score 850; DB 6; Length 162;
Best Local Similarity 98.8%; Pred. No. 2, 2e-90;
Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 MKGFTATLFLMTLIFPSCSGGGKAMPYHVCSDSGLVLYQSCDPLQDFGFSVEKCSK 60
DB 1 MKGFTATLFLMTLIFPSCSGGGKAMPYHVCSDSGLVLYQSCDPLQDFGFSVEKCSK 60
QY 61 QLKSNINIRFGIILREDIKELFLDLALMSGSSVYNFSYPCIALPKFSFGRRKGEQI 120
DB 61 QLKSNINIRFGIILREDIKELFLDLALMSGSSVYNFSYPCIALPKFSFGRRKGEQI 120
QY 121 YYAGPVNNPEFTIPQGEYQVLELYTEKSTVACANATIMCS 162
DB 121 YYAGPVNNPEFTIPQGEYQVLELYTEKSTVACANATIMCS 162
XX
RESULT 6
AAV84000
ID AAV84000 standard; protein; 162 AA.
XX
AC AAV84000;
XX
DT 25-OCT-2000 (first entry)
XX
DE Human B-cell surface protein MD-1.
XX
XX Human; B cell surface protein; apoptosis; antiallergic; allergy; EST;
XX antileukemic; immunosuppressive; dermatological; antiinflammatory;
XX autoimmune disease; asthma; atopic dermatitis; expressed sequence tag.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /note= "signal peptide"
FT Protein /note= "mature MD-1 protein"
XX
XX JP2000106880-A.
XX
XX 18-APR-2000.
XX
XX 08-OCT-1998; 98JP-00286470.
XX
XX 08-OCT-1998; 98JP-00286470.
XX
XX 08-OCT-1998; 98JP-00286470.
XX
XX (MITU) MITSUBISHI CHEM CORP.
XX
XX WPI: 2000-353476/31.
XX
XX N-PSDB; AAA11221.
XX
XX A new DNA encoding a human B cell surface protein, useful for treating
XX autoimmune diseases, allergic diseases, asthma and atopic dermatitis.
XX
PS Claim 1; Page 11; 12p; Japanese.

XX This sequence represents a human B cell surface protein, designated MD-1.
CC The protein is involved in the inhibition or induction of B cell
CC apoptosis and has antiallergic, antileukemic, immunosuppressive,
CC dermatological and antiinflammatory activity. The protein and the DNA are
CC used as treating and diagnostic agents for diseases related to antibody
CC production by B cells, e.g. autoimmune or allergic diseases, asthma and
CC atopic dermatitis. The coding sequence was isolated from a human EST
CC clone (GenBank accession number T84854)
XX
SQ Sequence 162 AA;
Query Match 87.9%; Score 758; DB 3; Length 162;
Best Local Similarity 88.9%; Pred. No. 1, 1e-79;
Matches 144; Conservative 3; Mismatches 15; Indels 0; Gaps 0;
XX
QY 1 MKGFTATLFLMTLIFPSCSGGGKAMPYHVCSDSGLVLYQSCDPLQDFGFSVEKCSK 60
DB 1 MKGFTATLFLMTLIFPSCSGGGKAMPYHVCSDSGLVLYQSCDPLQDFGFSVEKCSK 60
QY 61 QLKSNINIRFGIILREDIKELFLDLALMSGSSVYNFSYPCIALPKFSFGRRKGEQI 120
DB 61 QLKSNINIRFGIILREDIKELFLDLALMSGSSVYNFSYPCIALPKFSFGRRKGEQI 120
QY 121 YYAGPVNNPEFTIPQGEYQVLELYTEKSTVACANATIMCS 162
DB 121 YYAGPVNNPEFTIPQGEYQVLELYTEKSTVACANATIMCS 162
XX
RESULT 7
AAV13932
ID AAV13932 standard; protein; 162 AA.
XX
AC AAV13932;
XX
DT 14-JUL-1999 (first entry)
XX
DE Mouse CHP106 protein.
XX
XX CHP106; bacterial; viral; infection; cytokine activity; tissue formation;
XX cell proliferation; cell differentiation; immunostimulation; therapy;
XX immunosuppression; haematopoiesis control; tissue repair.
XX
XX Mus musculus.
XX
XX WO9918205-A1.
XX
XX 15-APR-1999.
XX
XX 06-OCT-1998; 98WO-JP004515.
XX
XX 07-OCT-1997; 97JP-00274673.
XX
XX (ONVOY) ONO PHARM CO LTD.
XX
XX Honjo T, Kato K, Tada H;
XX
XX WPI: 1999-277269/23.
XX
XX N-PSDB; AAX36693; AAX36694.
XX
XX New polypeptides useful in the treatment of various diseases including
XX bacterial and viral infections with cytokine activity.
XX
PS Claim 1; Page 44; 57p; Japanese.
XX
XX This sequence represents a CHP106 protein of the invention. The
XX polypeptides and their antibodies are applicable in drug compositions,
XX useful for treatment of various diseases including bacterial and viral
XX infections with cytokine activity, and activities e.g. on cell
XX proliferation/differentiation, immunostimulation/suppression, control of
XX haematopoiesis, and tissue formation and repair. The proteins and
XX antibodies have a wide spectrum of activities

SQ Sequence 162 AA;
 Query Match 71.1%; Score 613; DB 2; Length 162;
 Best Local Similarity 66.7%; Pred. No. 8.5e-63;
 Matches 108; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 1 MKGFTATLFLMTLIFPSCSGGGGKAMPYHVCSDSGLEVLVYQSCDPLQDFGFSVEKCK 60
 1 MNGVAAALVWILTSPPSSSDHSENGMPKHTACNSGLEGVYQSCDPLQDFGLSIDQCK 60
 DB 61 QKSNINIRFGIILREDIKELFDLALMSQSSVLTNFSYPICEALPKFSFGRRKGEQI 120
 61 QIOSNINIRFGIILREDIKELFDLALMSQSSVLTNFSYPICEALPKFSFGRRKGEQI 120
 QY 121 YVAGPVNPEFTIPQGEYQVLELYTEKSTVACANATIMCS 162
 121 YVAGPVNPEFTIPQGEYQVLELYTEKSTVACANATIMCS 162
 DB 121 YVAGPVNPEFTIPQGEYQVLELYTEKSTVACANATIMCS 162

RESULT 8
 ID AAY77481 standard; protein; 162 AA.
 AC AAY77481;
 DT 05-JUN-2000 (first entry)
 DE Rodent protein sequence, SEQ ID NO:50.
 XX Immune disorder; inflammation; allergy; immunosuppressant; antiarthritic;
 KM antirheumatoid; antiinflammatory; dermatological; antithyroid.
 XX Rodentia.
 OS WO200001817-A2.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-US012366.
 PF 06-JUL-1999; 98US-00110938.
 PR 13-JUL-1998; 98US-00114466.
 PR 23-JUL-1998; 98US-0093897P.
 PR 12-AUG-1998; 98US-00132968.
 PR 18-AUG-1998; 98US-00136214.
 PR 11-SEP-1998; 98US-0099999P.
 XX (SCHE) SCHERING CORP.
 PA Bates EM, Lebecque SJF, Murphy EE, Matteson JD, Gorman DM,
 PI Hedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA;
 PI Bazan JF, Mahony D, Lees EM;
 XX WPI; 2000-171015/15.
 DR New isolated mammalian genes, used to develop products for treating e.g.
 XX immune, inflammatory or allergic abnormalities, cancers or degenerative
 PT conditions.
 PT Disclosure; Page 208-209; 218pp; English.
 PS The invention relates to a number of primate and/or rodent proteins, and
 XX the genes which encode them. The invention encompasses human dendritic
 CC cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis factor)
 CC receptor family-related proteins HPTXA64, HSLJD37R and RANKL; human CC
 CC chemokine HCC5; human dendritic proteins Dub11 and Dub 12; human
 CC MD-1 and human and murine MD-2 proteins, which exhibit the properties of
 CC ligands for proteins comprising a leucine-rich motif (LRM); human cyclin
 CC E2; cDNAs encoding these proteins; and antibodies against these proteins.
 CC The proteins can be used for modulating the physiology or development of
 CC a cell. They can be used to mediate uptake of substrates (e.g.,
 CC prostaglandin-like molecules), to modulate or mediate cellular
 CC interactions (e.g., induce or prevent trafficking, proliferation, or

CC differentiation of cells), or are intracellular proteins which are
 CC important in various cellular processes such as the dendritic differentiation of
 CC proteins or cell cycle regulation. The products can be used for treating
 CC medical conditions such as immune, inflammatory or allergic disorders, or
 CC abnormal cellular proliferation, for example, cancers or degenerative
 CC conditions. They can be used to modulate immune responses in disease
 CC states e.g., autoimmune disorders, including rheumatoid arthritis, as well
 CC as systemic lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well
 CC as acute and chronic inflammatory responses in which T cell activation,
 CC expansion, and/or immunological T cell memory play an important role.
 CC Sequences AAY77463-Y77464, AAY77474-Y77475 and AAY77481 represent primate
 CC proteins of undefined function. AAY77462 and AAY77481 are rodent proteins
 CC of undefined function, and AAY77482 is an avian protein of undefined
 CC function. These sequences are given in the sequence listing but are not
 CC referred to in the remainder of the specification

SQ Sequence 162 AA;
 Query Match 71.1%; Score 613; DB 3; Length 162;
 Best Local Similarity 66.7%; Pred. No. 8.5e-63;
 Matches 108; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 1 MKGFTATLFLMTLIFPSCSGGGGKAMPYHVCSDSGLEVLVYQSCDPLQDFGFSVEKCK 60
 1 MNGVAAALVWILTSPPSSSDHSENGMPKHTACNSGLEGVYQSCDPLQDFGLSIDQCK 60
 DB 61 QKSNINIRFGIILREDIKELFDLALMSQSSVLTNFSYPICEALPKFSFGRRKGEQI 120
 61 QKSNINIRFGIILREDIKELFDLALMSQSSVLTNFSYPICEALPKFSFGRRKGEQI 120
 DB 61 QIOSNINIRFGIILREDIKELFDLALMSQSSVLTNFSYPICEALPKFSFGRRKGEQI 120
 QY 121 YVAGPVNPEFTIPQGEYQVLELYTEKSTVACANATIMCS 162
 121 YVAGPVNPEFTIPQGEYQVLELYTEKSTVACANATIMCS 162
 DB 121 YVAGPVNPEFTIPQGEYQVLELYTEKSTVACANATIMCS 162

RESULT 9
 ID ABU61846 standard; protein; 162 AA.
 AC ABU61846;
 DT 15-AUG-2003 (first entry)
 DE Mouse MD1.
 KM Mouse; MD1; cell development; tissue culture development.
 XX Mus sp.
 OS US2003028005-A1.
 PN 06-FEB-2003.
 PD 11-AUG-1999; 99US-00372348.
 PF 12-AUG-1998; 98US-0096328P.
 PR (BAZAN) BAZAN J F.
 PA Bazan JF;
 PI WPI; 2003-466159/44.
 DR New composition comprising HCC5, Dub11, Dub12, primate MD1 or MD2 or
 XX rodent MD2 polypeptide, useful for modulating physiology or development
 PT of a cell or tissue culture cells.
 PT Disclosure; Page 18; 77p; English.
 PS The invention relates to a novel chemokine, deubiquitination or cell
 XX surface protein. The composition is useful for modulating physiology or
 CC development of a cell or tissue culture cells. The present sequence
 CC represents the amino acid sequence of mouse MD1

XX Sequence 162 AA;
 XX Query Match 71.1%; Score 613; DB 6; Length 162;
 XX Best Local Similarity 66.7%; Pred. No. 8.5e-63;
 XX Matches 108; Conservative 22; Mismatches 32; Indels 0; Gaps 0;
 QY 1 MKGFTATLFLMTLIFPSCSGGGGKAMPYVVCSDSGLEVLVYQSCDPLDPFGFSVEKCSK 60
 DB 1 MNGVAAALVWLITSPSSDHGSENGMPKHTACNSGGLVYVQSCDPLDPFGSLIDQCSK 60
 QY 61 QLKSNINIRFGIILREDIKELFLDIALMQSGSSVYNFSPICEALPKFSFGRRKGEQI 120
 DB 61 QIQSNINIRFGIILRDIDRLFLDITLMKSSILNYSYPLCEBDQPKFSFGRRKGEQI 120
 QY 121 YYAGPVNNPEFTIPGEGYCVLTLELYTEKSTVACANATIMCS 162
 DB 121 YYAGPVNNPEGLDVPQGEYQLLLELYNENRATVACANATVTS 162
 RESULT 10
 ID ADE59272 standard; protein; 162 AA.
 AC ADE59272;
 AC ADE59272;
 DT 29-JAN-2004 (first entry)
 DE Rat Protein NP_034875, SEQ ID NO 5166.
 KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KM chronic constriction injury; CCI, spared nerve injury; SNI; Chung.
 OS Rattus norvegicus.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PF 14-AUG-2002; 2002WO-US025765.
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 PA (GENO) GEN HOSPITAL CORP.
 PA (PARB) BAYER AG.
 PI Woolf C, D'Urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; NP_034875.
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017P; English.
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 SQ Sequence 162 AA;
 XX Query Match 71.1%; Score 613; DB 7; Length 162;
 XX Best Local Similarity 66.7%; Pred. No. 8.5e-63;
 XX Matches 108; Conservative 22; Mismatches 32; Indels 0; Gaps 0;
 QY 1 MKGFTATLFLMTLIFPSCSGGGGKAMPYVVCSDSGLEVLVYQSCDPLDPFGFSVEKCSK 60
 DB 1 MNGVAAALVWLITSPSSDHGSENGMPKHTACNSGGLVYVQSCDPLDPFGSLIDQCSK 60
 QY 61 QLKSNINIRFGIILREDIKELFLDIALMQSGSSVYNFSPICEALPKFSFGRRKGEQI 120
 DB 61 QIQSNINIRFGIILRDIDRLFLDITLMKSSILNYSYPLCEBDQPKFSFGRRKGEQI 120
 QY 121 YYAGPVNNPEFTIPGEGYCVLTLELYTEKSTVACANATIMCS 162
 DB 121 YYAGPVNNPEGLDVPQGEYQLLLELYNENRATVACANATVTS 162
 RESULT 11
 ID AAY77482 standard; protein; 160 AA.
 AC AAY77482;
 AC AAY77482;
 DT 05-JUN-2000 (first entry)
 DE Avian protein sequence, SEQ ID NO:52.
 KM Immune disorder; inflammation; allergy; immunosuppressant; antiarthritic;
 KM antirheumatoid; antiinflammatory; dermatological; antithyroid.
 OS Aves.
 PN WO200001817-A2.
 PD 13-JAN-2000.
 PF 06-JUL-1999; 99WO-US012366.
 PR 06-JUL-1998; 98US-00110938.
 PR 13-JUL-1998; 98US-00114466.
 PR 23-JUL-1998; 98US-0093897P.
 PR 12-AUG-1998; 98US-00132968.
 PR 18-AUG-1998; 98US-00136214.
 PR 11-SEP-1998; 98US-0099999P.
 PA (SCHE) SCHERING CORP.
 PI Bates EM, Lebecque SJF, Murphy EE, Matson JD, Gorman DM;
 PI Hedrick JA, Wang L, Ziolklik A, Murgolo NJ, Greene JR, Johnston JA;
 PI Bazan JF, Mahony D, Lees EM;
 DR WPI; 2000-171015/15.
 DR N-PSDB; AA592421.
 PT New isolated mammalian genes, used to develop products for treating e.g.
 PT immune, inflammatory or allergic abnormalities, cancers or degenerative
 PT conditions.

PS Disclosure; Page 210-211; 218pp; English.

CC The invention relates to a number of primate and/or rodent proteins, and
 CC the genes which encode them. The invention encompasses human dendritic
 CC cell prostaglandin transporter (DC-PTP); the TNF (tumour necrosis factor)
 CC receptor family-related proteins HDTRA84, HSLUB37R and RANKL; human CC
 CC chemokine HCC5; human dendritic activating proteins Ddb1 and Ddb 12; human
 CC MD-1 and human and murine MD-2 proteins, which exhibit the properties of
 CC ligands for proteins comprising a leucine-rich motif (LRM); human cyclin
 CC E2; CDNA's encoding these proteins; and antibodies against these proteins.
 CC The proteins can be used for modulating the physiology or development of
 CC a cell. They can be used to mediate uptake of substrates (e.g.,
 CC prostaglandin-like molecules), to modulate or mediate cellular
 CC interactions (e.g., induce or prevent trafficking, proliferation, or
 CC differentiation of cells), or are intracellular proteins which are
 CC important in various cellular processes such as the deubiquitination of
 CC proteins or cell cycle regulation. The products can be used for treating
 CC medical conditions such as immune, inflammatory or allergic disorders, or
 CC abnormal cellular proliferation, for example, cancers or degenerative
 CC conditions. They can be used to modulate immune responses in disease
 CC states e.g., autoimmune disorders, including rheumatoid arthritis, as well
 CC systemic lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well
 CC as acute and chronic inflammatory responses in which T cell activation,
 CC expansion, and/or immunological T cell memory play an important role.
 CC Sequences AAY7463-Y77464, AAY7474-Y77475 and AAY77484 represent primate
 CC proteins of undefined function. AAY77462 and AAY77481 are rodent proteins
 CC of undefined function, and AAY77482 is an avian protein of undefined
 CC function. These sequences are given in the sequence listing but are not
 CC referred to in the remainder of the specification

CC Sequence 160 AA;

Query Match 39.0%; Score 336; DB 3; Length 160;

Best Local Similarity 44.4%; Pred. No. 1.4e-30; Indels 0; Gaps 0;

Matches 59; Conservative 26; Mismatches 48; Indels 0; Gaps 0;

QY 27 WPTHTVCSGSLGELYQSCDPLDPGFSYKSCSKOLKSNINIRFGILREDIKELFLDIA 86

DB 22 WPTHTVCKEENLEIYKSCDPODFAFSIDRCSDVTTHTFDIRAAVLRQSIKELYAKVD 81

QY 87 LMSQSSVYLNFSYICENALPKFSFGRRKGEQIYYAGPVNNPEFTIPQGEYQVLELYT 146

DB 82 LIINGKTVLSSETLIGPGSLKLIKCGKKGEHLVYEGPTTGKIKELPQDYYTTARLTN 141

QY 147 EKSTVACANATI 159

DB 142 EDRATVACADFTV 154

QY

RESULT 12

ABU61847

ABU61847 standard; protein; 160 AA.

ABU61847;

15-AUG-2003 (first entry)

Chicken MD1.

Chicken; MD1; cell development; tissue culture development.

Gallus gallus.

US2003028005-A1.

06-FEB-2003.

11-AUG-1999; 99US-00372348.

12-AUG-1998; 98US-0096328P.

(BAZA/) BAZAN J F.

PI Bazan JF;

DR WPI; 2003-466159/44.

DR N-PSDB; ACA62465.

PT New composition comprising HCC5, Ddb1, Ddb12, primate MD1 or MD2 or

PT rodent MD2 polypeptide, useful for modulating physiology or development

PT of a cell or tissue culture cells.

PS Disclosure; Page 18; 77pp; English.

CC The invention relates to a novel chemokine, de-ubiquitination or cell

CC surface protein. The composition is useful for modulating physiology or

CC development of a cell or tissue culture cells. The present sequence

CC represents the amino acid sequence of chicken MD1

CC Sequence 160 AA;

Query Match 39.0%; Score 336; DB 6; Length 160;

Best Local Similarity 44.4%; Pred. No. 1.4e-30; Indels 0; Gaps 0;

Matches 59; Conservative 26; Mismatches 48; Indels 0; Gaps 0;

QY 27 WPTHTVCSGSLGELYQSCDPLDPGFSYKSCSKOLKSNINIRFGILREDIKELFLDIA 86

DB 22 WPTHTVCKEENLEIYKSCDPODFAFSIDRCSDVTTHTFDIRAAVLRQSIKELYAKVD 81

QY 87 LMSQSSVYLNFSYICENALPKFSFGRRKGEQIYYAGPVNNPEFTIPQGEYQVLELYT 146

DB 82 LIINGKTVLSSETLIGPGSLKLIKCGKKGEHLVYEGPTTGKIKELPQDYYTTARLTN 141

QY 147 EKSTVACANATI 159

DB 142 EDRATVACADFTV 154

RESULT 13

AAV13929

AAV13929 standard; protein; 160 AA.

AAV13929;

14-JUL-1999 (first entry)

Mouse OHP106 protein.

OHP106; bacterial; viral; infection; cytokine activity; tissue formation;

KW cell proliferation; cell differentiation; immunostimulation; therapy;

KW immunosuppression; haematopoiesis control; tissue repair.

Mus musculus.

WO9918205-A1.

15-APR-1999.

06-OCT-1998; 98WO-JP004515.

07-OCT-1997; 97JP-00274673.

(ONVO) ONO PHARM CO LTD.

Honjo T, Kato K, Tada H;

WPI; 1999-277269/23.

N-PSDB; AAX36687, AAX36688.

New polypeptides useful in the treatment of various diseases including

bacterial and viral infections with cytokine activity.

Claim 1; Page 36-37; 57pp; Japanese.

This sequence represents a OHP106 protein of the invention. The

polypeptides and their antibodies are applicable in drug compositions,

CC useful for treatment of various diseases including bacterial and viral
 CC infections with cytokine activity, and activities e.g. on cell
 CC proliferation/differentiation, immunostimulation/suppression, control of
 CC haematopoiesis, and tissue formation and repair. The proteins and
 CC antibodies have a wide spectrum of activities

SC Sequence 160 AA:

Query Match 12.3%; Score 106; DB 2; Length 160;
 Best Local Similarity 26.3%; Pred. No. 0.00084;
 Matches 36; Conservative 24; Mismatches 61; Indels 16; Gaps 5;

QY 33 CSDSGLEVLVQSCDPIQ-DGFSVEKSKQKNSNINIRFGIILREDIKELFLDALMSQG 91
 DB 25 CNSSDAIISYCDHLKFPISISEPCIRLGTNGVHVEFIPRGKLYFNLFI---- 80
 QY 92 SSVLNFSYP-----ICBALPKFSGCGRRKGEQIYAGPVNNEFTIPQGEYQVLELY- 145
 DB 81 -SVNSIELPKRKEVLCHGHDDYSPCRALKGETVNTSIPFSPGILFPKGYRCVAEALA 139
 QY 146 --TEKSTVACANATIM 160
 DB 140 GDTTEK--LFCINFTII 154

RESULT 14

AAB35928
 ID AAB35928 standard; protein; 160 AA.

AC AAB35928;

DT 26-FEB-2001 (first entry)

DE Murine MD-2 amino acid sequence.

KW MD-2; immunosuppressant; allergy; asthma; atopic dermatitis; mouse;
 infection; prevention.

OS Mus musculus.

PN JP2000262290-A.

PD 26-SEP-2000.

XX 18-MAR-1999; 99JP-00073815.

PR 18-MAR-1999; 99JP-00073815.

PA (MITU) MITSUBISHI CHEM CORP.

DR WPI; 2000-682118/67.

DR N-PSDB; AAC66388.

PT A new protein controlling the infection-preventing reaction against a
 PT microbe.

PS Claim 2; Page 11-13; 14pp; Japanese.

CC This invention relates to a protein, MD-2, which controls an infection
 CC prevention reaction against a microbe. Protein and cDNA sequences
 CC AAC66387 - AAC66388 and AAB35927 - AAB35928 represent human and mouse MD-
 CC 2. MD-2 increases NF-kappaB activation through TLR4 molecules. The protein
 CC has immunosuppressant, anti-allergy; antiasthmatic and dermatological
 CC activity. The protein and the DNA can be used as a treating agent and a
 CC diagnostic agent for diseases such as autoimmune diseases, allergic
 CC diseases, asthma and atopic dermatitis

SC Sequence 160 AA:

Query Match 12.3%; Score 106; DB 3; Length 160;
 Best Local Similarity 26.3%; Pred. No. 0.00084;
 Matches 36; Conservative 24; Mismatches 61; Indels 16; Gaps 5;

QY 33 CSDSGLEVLVQSCDPIQ-DGFSVEKSKQKNSNINIRFGIILREDIKELFLDALMSQG 91
 DB 25 CNSSDAIISYCDHLKFPISISEPCIRLGTNGVHVEFIPRGKLYFNLFI---- 80
 QY 92 SSVLNFSYP-----ICBALPKFSGCGRRKGEQIYAGPVNNEFTIPQGEYQVLELY- 145
 DB 81 -SVNSIELPKRKEVLCHGHDDYSPCRALKGETVNTSIPFSPGILFPKGYRCVAEALA 139
 QY 146 --TEKSTVACANATIM 160
 DB 140 GDTTEK--LFCINFTII 154

RESULT 15

AAV13931
 ID AAV13931 standard; protein; 160 AA.

AC AAV13931;

DT 14-JUL-1999 (first entry)

DE Human OHP106 protein.

XX OHP106; bacterial; viral; infection; cytokine activity; tissue formation;
 KW cell proliferation; cell differentiation; immunostimulation; therapy;
 KW immunosuppression; haematopoiesis control; tissue repair.

OS Homo sapiens.

PN WO9918205-A1.

PD 15-APR-1999.

XX 06-OCT-1998; 98WO-JP004515.

PR 07-OCT-1997; 97JP-00274673.

PA (ONCO) ONO PHARM CO LTD.

PI Honjo T, Kato K, Tada H;

DR WPI; 1999-277269/23.

DR N-PSDB; AAX36691, AAX36692.

PT New polypeptides useful in the treatment of various diseases including
 PT bacterial and viral infections with cytokine activity.

PS Claim 1; Page 41-42; 57pp; Japanese.

CC This sequence represents a OHP106 protein of the invention. The
 CC polypeptides and their antibodies are applicable in drug compositions,
 CC useful for treatment of various diseases including bacterial and viral
 CC infections with cytokine activity, and activities e.g. on cell
 CC proliferation/differentiation, immunostimulation/suppression, control of
 CC haematopoiesis, and tissue formation and repair. The proteins and
 CC antibodies have a wide spectrum of activities

SC Sequence 160 AA:

Query Match 11.8%; Score 101.5; DB 2; Length 160;
 Best Local Similarity 24.1%; Pred. No. 0.0028;
 Matches 34; Conservative 26; Mismatches 70; Indels 11; Gaps 3;

QY 4 PPAITFLMTLIFPSSGGGKAWPTHVCSDSGLEVLVQSCDPIQ-DGFSVEKSKQL 62
 DB 6 FSTSLF--SSITF-----EAKQYVNCSSDASISYTCQKQYISINVPCLILK 55
 QY 63 KSNINIRFGIILREDIKELFLDALMSQSSVLNFSYPCBALPKFSGCGRRKGEQIY 122
 DB 56 GSKGLHIFYIPRRLIKOLYFNLVITVNTMLPKRKEVICGSDDDYSPCRALKGETVNT 115
 QY 123 AGPVNNEFTIPQGEYQVLE 143

Thu Apr 29 15:51:26 2004

us-09-899-917-2.rag

Page 9

Db 116 TISFSEKIKFSKGYKCYVE 136

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Job time : 60 secs

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OM protein - protein search, using sw model

Run on: April 29, 2004, 15:21:06 ; Search time 23 Seconds
(without alignments)
363,626 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	862	100.0	162 3 US-08-994-962-2	Sequence 2, Appl1
2	344	39.9	133 3 US-08-994-962-3	Sequence 3, Appl1
3	94	10.9	60 3 US-08-984-962-17	Sequence 17, Appl1
4	73.5	8.5	264 3 US-08-969-644-16	Sequence 16, Appl1
5	73.5	8.5	264 3 US-08-444-189-16	Sequence 16, Appl1
6	73.5	8.5	264 3 US-08-468-544-16	Sequence 16, Appl1
7	73.5	8.5	442 1 US-08-220-151-22	Sequence 22, Appl1
8	73.5	8.5	442 1 US-08-413-118-22	Sequence 22, Appl1
9	73.5	8.5	442 3 US-08-473-446-22	Sequence 22, Appl1
10	73.5	8.5	442 6 US-08-473-446-22	Sequence 22, Appl1
11	73.5	8.5	787 6 US-09-252-991A-26468	Sequence 26468, A
12	71.5	8.3	442 6 US-07-18-2	Patent No. 5470718
13	71.5	8.2	668 1 US-08-530-950-13	Sequence 13, Appl1
14	71.5	8.2	668 3 US-09-149-879-13	Sequence 13, Appl1
15	71.5	8.2	668 3 US-09-057-009-13	Sequence 13, Appl1
16	69.5	8.1	184 4 US-09-384-162-12	Sequence 12, Appl1
17	69.5	8.0	1012 4 US-09-285-385C-4	Sequence 4, Appl1
18	68	7.9	294 4 US-09-252-991A-27242	Sequence 27242, A
19	68	7.9	459 1 US-08-336-618-12	Sequence 12, Appl1
20	68	7.9	459 1 US-08-336-618-26	Sequence 26, Appl1
21	68	7.9	857 1 US-07-17-31F-2	Sequence 2, Appl1
22	67.5	7.8	204 4 US-09-134-001C-3617	Sequence 3617, Appl1
23	67.5	7.8	458 1 US-08-336-618-24	Sequence 24, Appl1
24	67.5	7.8	844 4 US-09-564-805-227	Sequence 227, Appl1
25	66.5	7.7	372 1 US-08-597-236-8	Sequence 8, Appl1
26	66.5	7.7	372 1 US-08-746-682A-8	Sequence 8, Appl1
27	66.5	7.7	793 2 US-08-468-558-5	Sequence 5, Appl1

28	66.5	7.7	793 3 US-08-676-444-5	Sequence 5, Appl1
29	66	7.7	494 3 US-09-205-283-12	Sequence 12, Appl1
30	66	7.7	2233 3 US-08-569-853-1	Sequence 1, Appl1
31	66	7.7	2233 3 US-08-569-853-2	Sequence 2, Appl1
32	66	7.7	2233 3 US-08-569-853-1	Sequence 1, Appl1
33	65.5	7.6	617 4 US-09-198-452A-155	Sequence 155, Appl1
34	65	7.5	379 4 US-09-491-577-4	Sequence 4, Appl1
35	65	7.5	484 1 US-08-030-096-8	Sequence 8, Appl1
36	65	7.5	1847 6 US-08-442-10	Patent No. 525642
37	65	7.5	1847 6 US-08-442-10	Patent No. 5472939
38	65	7.5	2039 6 US-08-442-10	Patent No. 525642
39	65	7.5	2039 6 US-08-442-10	Patent No. 5472939
40	65	7.5	2489 4 US-09-911-842A-5	Sequence 5, Appl1
41	64.5	7.5	511 3 US-09-201-641-2	Sequence 2, Appl1
42	64.5	7.5	511 4 US-09-323-998E-60	Sequence 60, Appl1
43	64.5	7.5	859 4 US-09-134-000C-6022	Sequence 6022, Appl1
44	64	7.4	483 3 US-09-108-020-16	Sequence 16, Appl1
45	64	7.4	3635 4 US-09-845-583A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-994-962-2
Sequence 2, Application US/08994962
Patent No. 6284486
GENERAL INFORMATION:
APPLICANT: Olsen, Henrik S.
TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSER: Sterne, Kessler Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,962
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,869
FILING DATE: 20-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/037,388
FILING DATE: 07-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET INFORMATION: 1488.0440002
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-994-962-2
Query Match 100.0%; Score 862; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 8e-100;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFTLTLEMTLIFSSGGGGGKAMPHVWCDSDGLVLYQSCDPLQDFPFVSKCK 60
DB 1 MGFTLTLEMTLIFSSGGGGGKAMPHVWCDSDGLVLYQSCDPLQDFPFVSKCK 60
QY 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVNFSPICEALPKFSFGRRKGEQI 120
DB 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVNFSPICEALPKFSFGRRKGEQI 120
QY 121 YVAGPVNPEFTIPQGEYQVLTLETKSTVACANATIMCS 162
DB 121 YVAGPVNPEFTIPQGEYQVLTLETKSTVACANATIMCS 162

RESULT 2

US-08-994-962-3
Sequence 3, Application US/08994962
Patent No. 6284486
GENERAL INFORMATION:
APPLICANT: Olsen, Henrik S.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,962
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,869
FILING DATE: 20-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/037,388
FILING DATE: 07-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0440002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-994-962-3

Query Match 39.9%; Score 344; DB 3; Length 133;

Best Local Similarity 45.1%; Pred. No. 4.2e-35;

Matches 60; Conservative 26; Mismatches 47; Indels 0; Gaps 0;

QY 27 WPTHVVCDSGLVLYQSCDPLQDFGFSVEKSKQKLNINIRFGIILREDIKELFLDLA 86
DB 1 WPTHVVCDSGLVLYQSCDPLQDFGFSVEKSKQKLNINIRFGIILREDIKELFLDLA 86
QY 87 LMSGSSVNFSPICEALPKFSFGRRKGEQIYVAGPVNPEFTIPQGEYQVLTLELYT 146
DB 87 LMSGSSVNFSPICEALPKFSFGRRKGEQIYVAGPVNPEFTIPQGEYQVLTLELYT 146

DB 61 LIINKTVLSYSELTICDPGLSKLIFCGKKKGEMHYEGPTLGIKBIPOGDYITLRLTN 120

QY 147 EKSTVACANATI 159
DB 121 EDRAIVACADPTV 133

RESULT 3

US-08-994-962-17
Sequence 17, Application US/08994962
Patent No. 6284486
GENERAL INFORMATION:
APPLICANT: Olsen, Henrik S.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,962
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,869
FILING DATE: 20-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/037,388
FILING DATE: 07-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0440002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-994-962-17

Query Match 10.9%; Score 94; DB 3; Length 60;

Best Local Similarity 33.3%; Pred. No. 0.00027;

Matches 43; Conservative 3; Mismatches 13; Indels 70; Gaps 11;

QY 27 WPTHVVCDSGLVLYQSCDPLQDFGFSVEKSKQKLNINIRFGIILREDIKELFLDLA 86
DB 1 WPTHVVCDSGLVLYQSCDPLQDFGFSVEKSKQKLNINIRFGIILREDIKELFLDLA 86
QY 87 LMSGSSVNFSPICEALPKFSFGRRKGEQIYVAGPVNPEFTIPQGEYQVLTLELYT 146
DB 30 -----GVLSTLKFQG--KGE--YGP-----IPG-----YL 52
QY 147 EKSTVACA 155
DB 53 ER--TVACA 59

RESULT 4
US-08-969-644-16; Sequence 16, Application US/08969644
; Patent No. 6096519

; GENERAL INFORMATION:

; APPLICANT: Ratti, Giulio

; APPLICANT: Comanducci, Maurizio

; APPLICANT: Tecce, Mario F.

; APPLICANT: Giuliani, Marzia M.

; TITLE OF INVENTION: PCDT PLASMID ISOLATED FROM CHLAMYDIA

; TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY

; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID

; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

; STREET: 301 N. Washington Street

; CITY: Falls Church

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22046-0747

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/969,644

; FILING DATE: 13-NOV-1997

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/467,152

; FILING DATE:

; APPLICATION NUMBER: US/07/661,820

; FILING DATE:

; APPLICATION NUMBER: IT MI 91A000314

; FILING DATE: 07-FEB-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Svensson, Leonard R.

; REGISTRATION NUMBER: 30,330

; REFERENCE/DOCKET NUMBER: 1267-202P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-241-1300

; TELEFAX: 703-241-2848

; TELEX: 248345

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 264 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-969-644-16

Query Match 8.5%; Score 73.5; DB 3; Length 264;

Best Local Similarity 27.6%; Pred. No. 0.83; 50; Indels 29; Gaps 5;

Matches 35; Conservative 13; Mismatches 50; Indels 29; Gaps 5;

; DB 10 LMTLIFSCGGGGGKAMPHTHYVCSDS---GLEVLVYSCDPLDQFGFSEVKCSKQKLSNT 66

; DB 1 LHTLVFCGFGGTGKTTLISLVGCTLAQFLGKVLADLDP-----QSNL 45

; DB 67 NIRFGILREDIKELFDLALMSQSSVLNFSYPICEA-----LPKFSFGRRKGEQIY 121

; DB 46 SSGIAGASVRSQKGLH-DIVYTSNDLKI-----ICETKDSVLLIPASFSSEQFREDLI 99

; DB 122 YAGPVNN 128

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; Sequence 16, Application US/08444189

; Patent No. 6110705

; GENERAL INFORMATION:

; APPLICANT: Ratti, Giulio

; APPLICANT: Comanducci, Maurizio

; APPLICANT: Tecce, Mario F.

; APPLICANT: Giuliani, Marzia M.

; TITLE OF INVENTION: PCDT PLASMID ISOLATED FROM CHLAMYDIA

; TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY

; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID

; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

; STREET: 301 N. Washington Street

; CITY: Falls Church

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22046-0747

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/444,189

; FILING DATE:

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/180,528

; FILING DATE:

; APPLICATION NUMBER: US/07/991,512

; FILING DATE:

; APPLICATION NUMBER: US/07/661,820

; FILING DATE:

; APPLICATION NUMBER: IT MI 91A000314

; FILING DATE: 07-FEB-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Svensson, Leonard R.

; REGISTRATION NUMBER: 30,330

; REFERENCE/DOCKET NUMBER: 1267-202P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-241-1300

; TELEFAX: 703-241-2848

; TELEX: 248345

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 264 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-444-189-16

Query Match 8.5%; Score 73.5; DB 3; Length 264;

Best Local Similarity 27.6%; Pred. No. 0.83; 50; Indels 29; Gaps 5;

Matches 35; Conservative 13; Mismatches 50; Indels 29; Gaps 5;

; DB 10 LMTLIFSCGGGGGKAMPHTHYVCSDS---GLEVLVYSCDPLDQFGFSEVKCSKQKLSNT 66

; DB 1 LHTLVFCGFGGTGKTTLISLVGCTLAQFLGKVLADLDP-----QSNL 45

; DB 67 NIRFGILREDIKELFDLALMSQSSVLNFSYPICEA-----LPKFSFGRRKGEQIY 121

; DB 46 SSGIAGASVRSQKGLH-DIVYTSNDLKI-----ICETKDSVLLIPASFSSEQFREDLI 99

; DB 122 YAGPVNN 128

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

; DB 100 HRGPSNN 106

RESULT 6
US-08-468-544-16

; Sequence 16, Application US/08468544

```

; Patent No. 6248563
; GENERAL INFORMATION:
; APPLICANT: Ratti, Giulio
; APPLICANT: Comanducci, Maurizio
; APPLICANT: Tecce, Mario F.
; APPLICANT: Giuliani, Marzia M.
; TITLE OF INVENTION: PCID PLASMID ISOLATED FROM CHLAMYDIA
; TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
; TITLE OF INVENTION: THEM, RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 301 N. Washington Street
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,544
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/661,820
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: IT MI 91A000314
; FILING DATE: 07-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Swensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1267-202P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-544-16

Query Match      8.5%; Score 73.5; DB 3; Length 264;
Best Local Similarity 27.6%; Pred. No. 0.83; 50; Indels 29; Gaps 5;
Matches 35; Conservative 13; Mismatches 5;

QY 10 LMTLIFPSCGGGKAMPHTVVCSDS---GLEVLYOSCDPLDFGFSVEKCSKQLKSN1 66
DB 1 LHTLVFSCFKGRTKTLNLCVGNLAFGLKXVTLADLP-----QSNL 45
QY 67 NIRFGIILREDIKELFDLALMSGSSVLMFSYPICEAA-----LPKFSGCRKKEQIY 121
DB 46 SSGIGASVRSQDKGLH-DIVYTSNDKSI-----ICETKDSVLLIPASFSSEQFRELLI 99
QY 122 YAGPVNN 128
DB 100 HRGPSNN 106

RESULT 7
US-08-220-151-22
; Sequence 22, Application US/08220151
; Patent No. 5529780
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Limbach, Keith J.
; TITLE OF INVENTION: NOCLOBOTIDE AND AMINO ACID SEQUENCES OF

```

```

; TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC AND gD AND USES THEREFOR
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,151
; FILING DATE: 30-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2540
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066 CURTMS
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 442 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; US-08-220-151-22

Query Match      8.5%; Score 73.5; DB 1; Length 442;
Best Local Similarity 25.4%; Pred. No. 1.7;
Matches 43; Conservative 17; Mismatches 62; Indels 47; Gaps 8;

QY 2 KGFTATLFTLTFPSCGGGKAMPHTVVCSDGLEVLYOSCDPLDFGFSVEKCSKQ 61
DB 161 KTYSKRL-TWPKIMPTC-----ATPIH-----DVGVMKNPFLSTRMDE----- 199
QY 62 LKSNINIRFGIT--LREDIKELFDLALMSGSSVL-----NFSYPICEAA 105
DB 200 -RSDILMQASLITAAETDDELGLVLAAPAHASAGLYRVLIEDGRRIYTDFTSPSER 258
QY 106 LP-----KFSFCGRKKEQIYAGPVNN---PEFTIPQSGYCVLLELY 145
DB 259 CFIAPELNFGNDRCKTPEQYSRGEVFTRRRLGFEFNPOGHEHMTWVFW 307

RESULT 8
US-08-413-118-22
; Sequence 22, Application US/08413118
; Patent No. 5688920
; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: LIMBACH, KEITH J.
; TITLE OF INVENTION: NOCLOBOTIDE AND AMINO ACID SEQUENCES OF
; TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC, gD AND gD AND USES THEREFOR
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE, 25TH FLOOR
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

Page 5

```

NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-473-446-22

Query Match 8.5%; Score 73.5; DB 3; Length 442;
Best Local Similarity 25.4%; Pred. No. 1.7;
Matches 43; Conservative 17; Mismatches 62; Indels 47; Gaps 8;

Cy 2 KQPTATPLMTLIPSCGGGGGKAWPTHVVCSDSLGLTYGSCDPLDQFGSVYKCKQ 61
Db 161 KYTSARL-TWFKIMPTC-----ATPIH-----DVSYMKCNFKLSFANCD-----199
Cy 62 LKSNINIRFGII--LREDIKELFDLALMSGSSVL-----NFSYPICEAA 105
Db 200 -RSDILMQASLITWAAETDDELGLVLAAPAHSAAGLYRVIETDGRRIYTDFTVIPSRR 258
Cy 106 LP-----KSFQGRKRGEOIYYAGPVNN-----PEFTIPQSEYVLELY 145
Db 259 CPIAFELNFGNDPCKTPEQYSRGEVFTTRRFLGSEFNPQGEHMTWVFW 307

RESULT 10
5470718-3
Patent No. 5470718
APPLICANT: O'CALLAGHAN, DENNIS J.
TITLE OF INVENTION: EQUINE HERPESVIRUS TYPE 1 GLYCOPROTEIN
ID NUCLEIC ACIDS
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/954,417
FILING DATE: 30-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 561,553
FILING DATE: 01-AUG-1990
SEQ ID NO:3:
LENGTH: 442
5470718-3

Query Match 8.5%; Score 73.5; DB 6; Length 442;
Best Local Similarity 25.4%; Pred. No. 1.7;
Matches 43; Conservative 17; Mismatches 62; Indels 47; Gaps 8;

Cy 2 KQPTATPLMTLIPSCGGGGGKAWPTHVVCSDSLGLTYGSCDPLDQFGSVYKCKQ 61
Db 161 KYTSARL-TWFKIMPTC-----ATPIH-----DVSYMKCNPLSPANCD-----199
Cy 62 LKSNINIRFGII--LREDIKELFDLALMSGSSVL-----NFSYPICEAA 105
Db 200 -RSDILMQASLITWAAETDDELGLVLAAPAHSAAGLYRVIETDGRRIYTDFTVIPSRR 258
Cy 106 LP-----KSFQGRKRGEOIYYAGPVNN-----PEFTIPQSEYVLELY 145
Db 259 CPIAFELNFGNDPCKTPEQYSRGEVFTTRRFLGSEFNPQGEHMTWVFW 307

RESULT 11
US-09-252-991A-26468
Sequence 26468 Application US/09252991A
Patent No. 6531795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

```


TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIORITY APPLICATION NUMBER: US 60/074,788
PRIORITY FILING DATE: 1998-02-18
PRIORITY APPLICATION NUMBER: US 60/094,190
PRIORITY FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26468
LENGTH: 787
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26468

Query Match 8.5%; Score 73; DB 4; Length 787;
Best Local Similarity 22.3%; Pred. No. 4.6;
Matches 27; Conservative 14; Mismatches 46; Indels 34; Gaps 3;

QY 10 LMTLIFPSCGGGGGKAMPTHTVVC-----SDSGHEVL-----YQS 44
DB 273 LMTLIRGKDDGGRRTTIKSMCRITPTGPVABRLNDPGEFLATLVNVSEPTNL 332

QY 45 CDPLDGFSEVKCSKQLKSNINIRFGI-----ILREDIKELFLDLALMSQSSVL 95
DB 333 MDKAGDVFSDRQKRMERSMANIEFGFGEQYQPTFEIRQCPNGVFDLLVVDGHEVK 392

QY 96 N 96
DB 393 N 393

RESULT 12
5470718-2
PATENT NO. 5470718
TITLE OF INVENTION: BOVINE HERPESVIRUS TYPE 1 GLYCOPROTEIN
ID NUCLEIC ACIDS
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/954,417
FILING DATE: 30-SEP-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 561,553
FILING DATE: 01-AUG-1990
SEQ ID NO: 2
LENGTH: 442

Query Match 8.3%; Score 71.5; DB 6; Length 442;
Best Local Similarity 25.4%; Pred. No. 3.1;
Matches 43; Conservative 16; Mismatches 63; Indels 47; Gaps 8;

QY 2 KGFATLFLWTLIFPSCGGGGKAMPTHTVVCSDSGHEVLVYOSCDPLDGFSEVKCSKQ 61
DB 161 KTYPARL-TWFKIMPTC-----ATPIH-----DVSVMCNPRLSFAMCDE----- 199

QY 62 LKSNINIRFGI--LRREDIKELFLDLALMSQSSVL-----NFSYPICEAA 105
DB 200 -RSDILMQASLITMAATDELDGLVLAAPASASGLRRVIEIDGRRIYTDFTSPSER 258

QY 106 LP-----KFSFGRRKGEQIYVAGPVNN-----PEFTIPOGEYVLTLELY 145
DB 259 CPAAFEAFNGPDRCKTPEQSRGEVFTRRFLGSEFNPQGEHMTWAKFM 307

RESULT 13
US-08-530-950-13
Sequence 13, Application US/08530950
Patent No. 5736381
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.

APPLICANT: Rainsaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Deltjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,950
FILING DATE: 19-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-530-950-13

Query Match 8.2%; Score 71; DB 1; Length 668;
Best Local Similarity 24.3%; Pred. No. 6.4;
Matches 33; Conservative 24; Mismatches 61; Indels 18; Gaps 5;

QY 28 PTHVCSDSGLVLYOSCDPLDGFSEVKCSKQLKSNINIRFGIILREDIKELFLDLAL 87
DB 488 PTHLCSAN-----QGTVKLCDPVSGLNVLASIAKTNIGCQ--SYMAPERIKSLNPDRA 540

QY 88 MSQSSVLNFSYPICEALPKFSFGRRKGEQIY--YAGPVNPEFTIPOGEY----- 138
DB 541 YTVGSDIWSLGLSTLEMLAGRYR--PPETVYNISQLSAIVDGPRLPSDKFSSDAQDF 599

QY 139 -QVLLLEYTKRSTYA 153
DB 600 VSLCLQKIPERRPTYA 615

RESULT 14
US-09-148-879-13
Sequence 13, Application US/09148879
Patent No. 6174676
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Rainsaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Deltjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,879
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-09-149-879-13

Query Match 8.2%; Score 71; DB 3; Length 668;
Best Local Similarity 24.3%; Pred. No. 6.4;
Matches 33; Conservative 24; Mismatches 61; Indels 18; Gaps 5;

QY 28 PTHVCSGSLGVLYQSCDPLQDFGFSVEKSKQKSNINIRGIIREDIKELFLDLAL 87
DB 488 PTNIIICSN-----QGTWKLCDFGVSGNIVASLAKTNIGCQ-SYVAPERIKSLNPDRA 540

QY 88 MSGSSVNFSPYPCIEALPKFSFCGRKGEQY--YAGPVNNEFTIPOGEY----- 138
DB 541 YTVQSDIWSLGLSLLEMLAKRIPY-PPEYDNIFQSLSAIVDGPRLPSDQSSDAQDF 599

QY 139 -QVLLLEYTEKSTVA 153
DB 600 VSLCLQKIPERRPTVA 615

RESULT 15
US-09-057-009-13
Sequence 13, Application US/09057009
Patent No. 6541605
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Raingeaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Derijard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,009
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
STRANDEDNESS: No. 6541605 Relevant
TOPOLOGY: linear
US-09-057-009-13

Query Match 8.2%; Score 71; DB 4; Length 668;
Best Local Similarity 24.3%; Pred. No. 6.4;
Matches 33; Conservative 24; Mismatches 61; Indels 18; Gaps 5;

QY 28 PTHVCSGSLGVLYQSCDPLQDFGFSVEKSKQKSNINIRGIIREDIKELFLDLAL 87
DB 488 PTNIIICSN-----QGTWKLCDFGVSGNIVASLAKTNIGCQ-SYVAPERIKSLNPDRA 540

QY 88 MSGSSVNFSPYPCIEALPKFSFCGRKGEQY--YAGPVNNEFTIPOGEY----- 138
DB 541 YTVQSDIWSLGLSLLEMLAKRIPY-PPEYDNIFQSLSAIVDGPRLPSDQSSDAQDF 599

QY 139 -QVLLLEYTEKSTVA 153
DB 600 VSLCLQKIPERRPTVA 615

Search completed: April 29, 2004, 15:23:47
Job time : 23 secs

Thu Apr 29 15:51:27 2004

us-09-899-917-2.rapb

Page 1

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OM protein - protein search, using sw model

Run on: April 29, 2004, 15:23:51 ; Search time 42 Seconds
(without alignments)
1069.160 Million cell updates/sec

Title: US-09-899-917-2

Perfect score: 862
Sequence: 1 MKGFATLFLWTLIFPSCSG.....ELYTEKSTVACANATIMCS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	862	100.0	162	9	US-09-899-917-2
2	862	100.0	162	12	US-10-000-066-13
3	860	98.6	162	10	US-09-372-348-19
4	613	71.1	162	10	US-09-372-348-27
5	613	71.1	162	12	US-10-000-066-10
6	344	39.9	133	9	US-09-899-917-3
7	336	39.0	160	10	US-09-372-348-29
8	106	12.3	160	12	US-10-000-066-1
9	101.5	11.8	160	10	US-09-372-348-23
10	101.5	11.8	160	12	US-10-000-066-7
11	96.5	11.2	160	10	US-09-372-348-26
12	94	10.9	60	9	US-09-899-917-17
13	81.5	9.5	555	12	US-10-424-599-214951
14	81	9.4	170	12	US-10-424-599-199134
15	78	9.0	876	12	US-10-282-122A-77326

16	76.5	8.9	1177	12	US-10-282-122A-45910	Sequence 45910, A
17	75.5	8.8	342	12	US-10-282-122A-54490	Sequence 54490, A
18	75.5	8.8	1241	12	US-10-282-122A-51957	Sequence 51957, A
19	75	8.7	505	14	US-10-205-823-427	Sequence 427, App
20	75	8.7	505	14	US-10-354-358-98	Sequence 98, Appl
21	75	8.7	522	12	US-10-087-193-84	Sequence 84, Appl
22	75	8.7	524	9	US-09-925-300-1538	Sequence 1538, Ap
23	72.5	8.4	1172	12	US-10-363-616-446	Sequence 446, App
24	72.5	8.4	1178	12	US-10-363-616-445	Sequence 445, App
25	72	8.4	266	12	US-10-425-114-53807	Sequence 53807, A
26	72	8.4	266	12	US-10-425-114-53809	Sequence 53809, A
27	72	8.4	266	12	US-10-425-114-68478	Sequence 68478, A
28	71.5	8.3	313	15	US-10-041-615-28	Sequence 28, Appl
29	71	8.2	668	9	US-09-761-569-13	Sequence 13, Appl
30	71	8.2	668	9	US-09-801-368-238	Sequence 238, Appl
31	71	8.2	668	14	US-10-081-119-20	Sequence 20, Appl
32	71	8.2	668	15	US-10-369-493-22148	Sequence 22148, A
33	71	8.2	1115	14	US-10-260-715-6	Sequence 6, Appl
34	71	8.2	1151	14	US-10-260-715-4	Sequence 4, Appl
35	70.5	8.2	114	10	US-09-372-348-25	Sequence 25, Appl
36	70.5	8.2	114	12	US-10-000-066-4	Sequence 4, Appl
37	70.5	8.2	218	12	US-10-335-977-6276	Sequence 6276, Ap
38	70.5	8.2	495	12	US-10-424-599-234625	Sequence 234625, A
39	70	8.1	215	12	US-10-282-122A-77503	Sequence 77503, A
40	70	8.1	291	15	US-10-264-237-1641	Sequence 1641, Ap
41	70	8.1	462	11	US-09-833-245-1692	Sequence 1692, Ap
42	70	8.1	515	15	US-10-369-493-17475	Sequence 17475, A
43	70	8.1	950	15	US-10-369-493-21918	Sequence 21918, A
44	69.5	8.1	191	12	US-10-424-599-234053	Sequence 234053, A
45	69.5	8.1	373	15	US-10-434-418-2	Sequence 2, Appl

ALIGNMENTS

Handwritten signature

RESULT 1
US-09-899-917-2
Sequence 2, Application US/09899917
Patent No. US20020119552A1
GENERAL INFORMATION:
APPLICANT: Olsen, Henrik S.
TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899, 917
FILING DATE: 09-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/994, 962
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/037, 388
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36, 688
REFERENCE/DOCKET NUMBER: 1488, 0440002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-899-917-2

Query Match 100.0%; Score 862; DB 9; Length 162;
Best Local Similarity 100.0%; Pred. No. 1,8e-93;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKGFTATLFLMTLIFPSGSGGGKAMPYHVCSDSGLVLYQSCDPLQDFGFSVEKCSK 60
DB 1 MKGFTATLFLMTLIFPSGSGGGKAMPYHVCSDSGLVLYQSCDPLQDFGFSVEKCSK 60
QY 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVYNFSYPICBALPKFSFGRRKGEQI 120
DB 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVYNFSYPICBALPKFSFGRRKGEQI 120
QY 121 YYAGPVNNEPFTIPQGEYQVLLLEYTEKRSIVACANATIMCS 162
DB 121 YYAGPVNNEPFTIPQGEYQVLLLEYTEKRSIVACANATIMCS 162

RESULT 2

US-10-000-066-13
Sequence 13, Application US/10000066
Publication No. US20020086364A1
GENERAL INFORMATION:
APPLICANT: HONJO, TOSUKU
APPLICANT: KATO, KEIZO
APPLICANT: YADA, HIDEAKI
TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE SAME, AND USE OF THEM
FILE REFERENCE: 058771
CURRENT APPLICATION NUMBER: US/10/000,066
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/529,064
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: PCT/JP98/04515
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: HEI-9-274673
PRIOR FILING DATE: 1997-10-07
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-000-066-13

had date

Query Match 100.0%; Score 862; DB 12; Length 162;
Best Local Similarity 100.0%; Pred. No. 1,8e-93;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKGFTATLFLMTLIFPSGSGGGKAMPYHVCSDSGLVLYQSCDPLQDFGFSVEKCSK 60
DB 1 MKGFTATLFLMTLIFPSGSGGGKAMPYHVCSDSGLVLYQSCDPLQDFGFSVEKCSK 60
QY 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVYNFSYPICBALPKFSFGRRKGEQI 120
DB 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVYNFSYPICBALPKFSFGRRKGEQI 120
QY 121 YYAGPVNNEPFTIPQGEYQVLLLEYTEKRSIVACANATIMCS 162
DB 121 YYAGPVNNEPFTIPQGEYQVLLLEYTEKRSIVACANATIMCS 162

RESULT 3
US-09-372-348-19
Sequence 19, Application US/09372348A
Publication No. US20030028005A1
GENERAL INFORMATION:

APPLICANT: Hedrick, Joseph A.
APPLICANT: Wang, Luquan
APPLICANT: Zlotnick, Albert
APPLICANT: Murgolo, Nicholas J.
APPLICANT: Greene, Jonathan R.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods
FILE REFERENCE: DX0884K(2d)
CURRENT APPLICATION NUMBER: US/09/372,348A
CURRENT FILING DATE: 1999-08-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 162
TYPE: PRT
ORGANISM: primate
US-09-372-348-19

Query Match 98.6%; Score 850; DB 10; Length 162;
Best Local Similarity 98.8%; Pred. No. 4,8e-92;
Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKGFTATLFLMTLIFPSGSGGGKAMPYHVCSDSGLVLYQSCDPLQDFGFSVEKCSK 60
DB 1 MKGFTATLFLMTLIFPSGSGGGKAMPYHVCSDSGLVLYQSCDPLQDFGFSVEKCSK 60
QY 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVYNFSYPICBALPKFSFGRRKGEQI 120
DB 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVYNFSYPICBALPKFSFGRRKGEQI 120
QY 121 YYAGPVNNEPFTIPQGEYQVLLLEYTEKRSIVACANATIMCS 162
DB 121 YYAGPVNNEPFTIPQGEYQVLLLEYTEKRSIVACANATIMCS 162

RESULT 4

US-09-372-348-27
Sequence 27, Application US/09372348A
Publication No. US20030028005A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
APPLICANT: Wang, Luquan
APPLICANT: Zlotnick, Albert
APPLICANT: Murgolo, Nicholas J.
APPLICANT: Greene, Jonathan R.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods
FILE REFERENCE: DX0884K(2d)
CURRENT APPLICATION NUMBER: US/09/372,348A
CURRENT FILING DATE: 1999-08-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 162
TYPE: PRT
ORGANISM: rodent
US-09-372-348-27

Query Match 71.1%; Score 613; DB 10; Length 162;
Best Local Similarity 66.7%; Pred. No. 5e-64;
Matches 108; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 1 MKGFTATLFLMTLIFPSGSGGGKAMPYHVCSDSGLVLYQSCDPLQDFGFSVEKCSK 60
DB 1 MKGFTATLFLMTLIFPSGSGGGKAMPYHVCSDSGLVLYQSCDPLQDFGFSVEKCSK 60
QY 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVYNFSYPICBALPKFSFGRRKGEQI 120
DB 61 QKSNINIRFGIILREDIKELFLDLALMSGSSVYNFSYPICBALPKFSFGRRKGEQI 120
QY 121 YYAGPVNNEPFTIPQGEYQVLLLEYTEKRSIVACANATIMCS 162
DB 121 YYAGPVNNEPFTIPQGEYQVLLLEYTEKRSIVACANATIMCS 162

Db 121 YVAGPVNNPGLDVGQGEYQLLLELYNNRATVACANATVTS 162

RESULT 5
US-10-000-066-10

Sequence 10, Application US/10000066
Publication No. US20020086364A1
GENERAL INFORMATION:
APPLICANT: HONDO, TASUKU
APPLICANT: KATO, KEIZO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE SAME, AND USE OF THEM
FILE REFERENCE: Q88771
CURRENT APPLICATION NUMBER: US/10/000,066
CURRENT FILING DATE: 2001-12-04
PRIORITY APPLICATION NUMBER: 09/529,064
PRIORITY FILING DATE: 2000-04-17
PRIORITY APPLICATION NUMBER: PCT/JP98/04515
PRIORITY FILING DATE: 1998-10-06
PRIORITY APPLICATION NUMBER: HEI-9-274673
PRIORITY FILING DATE: 1997-10-07
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 162
TYPE: PRT
ORGANISM: Mus musculus
US-10-000-066-10

Query Match 71.1%; Score 613; DB 12; Length 162;
Best Local Similarity 66.7%; Pred. No. 5e-64;
Matches 108; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 1 MKGFTAILFLMTLTFPSCGGGGKAMPTHYVCSDSGLVLYQSCDPLQDFGSEVEKCSK 60
DB 1 MGVVAAALLVWLITPSSSDHSGWPKHTACNSGGLEVVYQSCDPLQDFGLIDCSK 60
QY 61 QLSKINIRFGIILREDIKELFLDLALMSQSSVINFSPICFALPKFSFCGRKSGEQI 120
DB 61 QLSKINIRFGIILREDIKELFLDLALMSQSSVINFSPICFALPKFSFCGRKSGEQI 120
QY 121 YVAGPVNNPGLDVGQGEYQLLLELYNNRATVACANATVTS 162
DB 121 YVAGPVNNPGLDVGQGEYQLLLELYNNRATVACANATVTS 162

RESULT 6

US-09-899-917-3
Sequence 3, Application US/09899917
Patent No. US20020119552A1
GENERAL INFORMATION:
APPLICANT: Olsen, Henrik S.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,917
FILING DATE: 09-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/994,962
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/037,388
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1468.0440002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: NO. US20020119552A1 Relevant
TOPOLOGY: NO. US20020119552A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-899-917-3

Query Match 39.9%; Score 344; DB 9; Length 133;
Best Local Similarity 45.1%; Pred. No. 2.4e-32;
Matches 60; Conservative 26; Mismatches 47; Indels 0; Gaps 0;

QY 27 WPTHVCSDSGLVLYQSCDPLQDFGSEVEKCSKQLKSNINIRFGIILREDIKELFLDLA 96
DB 1 WPTHVCSDSGLVLYQSCDPLQDFGSEVEKCSKQLKSNINIRFGIILREDIKELFLDLA 96
QY 87 LMSQSSVINFSPICFALPKFSFCGRKSGEQIYVAGPVNNPGLDVGQGEYQLLLELYT 146
DB 61 LMSQSSVINFSPICFALPKFSFCGRKSGEQIYVAGPVNNPGLDVGQGEYQLLLELYT 120
QY 147 EKRSVACANATI 159
DB 121 EKRSVACANATI 133

RESULT 7

US-09-372-348-29
Sequence 29, Application US/09372348A
Publication No. US20030028005A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
APPLICANT: Wang, Luquan
APPLICANT: Zlotnik, Albert
APPLICANT: Murgolo, Nicholas J.
APPLICANT: Greene, Jonathan R.
APPLICANT: Johnston, James A.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods
FILE REFERENCE: DX084K(2d)
CURRENT APPLICATION NUMBER: US/09/372,348A
CURRENT FILING DATE: 1999-08-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 160
TYPE: PRT
ORGANISM: ayes
US-09-372-348-29

Query Match 39.0%; Score 336; DB 10; Length 160;
Best Local Similarity 44.4%; Pred. No. 2.8e-31;
Matches 59; Conservative 26; Mismatches 46; Indels 0; Gaps 0;

QY 27 WPTHVCSDSGLVLYQSCDPLQDFGSEVEKCSKQLKSNINIRFGIILREDIKELFLDLA 86
DB 22 WPTHVCSDSGLVLYQSCDPLQDFGSEVEKCSKQLKSNINIRFGIILREDIKELFLDLA 81
QY 87 LMSQSSVINFSPICFALPKFSFCGRKSGEQIYVAGPVNNPGLDVGQGEYQLLLELYT 146
DB 82 LMSQSSVINFSPICFALPKFSFCGRKSGEQIYVAGPVNNPGLDVGQGEYQLLLELYT 141

QY 147 EKSTVACANNT 159
DB 142 EDRAIVACADFTV 154

RESULT 8

US-10-000-066-1
; Sequence 1, Application US/10000066
; Publication No. US20020086364A1
; GENERAL INFORMATION:
; APPLICANT: HONJO, TASUKU
; APPLICANT: KATO, KEIZO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE SAME, AND USE OF THEM
; FILE REFERENCE: Q58771
; CURRENT APPLICATION NUMBER: US/10/000,066
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/529,064
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: PCT/JP98/04515
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: HEI-9-274673
; PRIOR FILING DATE: 1997-10-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-000-066-1

Query Match 12.3%; Score 106; DB 12; Length 160;
Best Local Similarity 26.3%; Pred. No. 0.00044;
Matches 36; Conservative 24; Mismatches 61; Indels 16; Gaps 5;

QY 33 CDSGLEVLVYQSCDPLQ-DGFSVEKSKOLKSNINIRFGILIRREDIKELFDLALMSG 91
DB 25 CNSSDAIISSYCDHLKFPISISEPCIRLGTNGFVHVEFIRGNLKYENLF- 80
QY 92 SSYLNFSYP-----ICEALPKFSFCGRKGEQIYYAGPVNNEFTIPQGEYQVLE- 145
DB 81 -SVNSILPRKREVLCHGHDDVDFCRALKGETVNTNISFSPGILFPKGYHCVAEATA 139
QY 146 --TEKSTVACANNTIM 160
DB 140 GDTEER--LFCNLFTII 154

RESULT 9

US-09-372-348-23
; Sequence 23, Application US/09372348A
; Publication No. US2003002805A1
; GENERAL INFORMATION:
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Wang, Luquan
; APPLICANT: Zlotnick, Albert
; APPLICANT: Murgolo, Nicholas J.
; APPLICANT: Greene, Jonathan R.
; APPLICANT: Johnston, James A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods
; FILE REFERENCE: DX084K(2d)
; CURRENT APPLICATION NUMBER: US/09/372,348A
; CURRENT FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 160
; TYPE: PRT
; ORGANISM: primate
US-09-372-348-23

Query Match 11.8%; Score 101.5; DB 10; Length 160;
Best Local Similarity 24.1%; Pred. No. 0.0015;
Matches 34; Conservative 26; Mismatches 70; Indels 11; Gaps 3;

QY 4 FTATLFLMTLIPSGCGGKAMPYHVCSDSGLEVLVYQSCDPLQ-DGFSVEKSKOL 62
DB 6 FFSFLF--SSIFL-----EAQKYVNCSSDASISYTCDMQYPIISINVPICIELK 55
QY 63 KSNINIRFGILIRREDIKELFDLALMSGSSVNLFSYPCALPKFSFCGRKGEQIY 122
DB 56 GSKGLHIFYPREDLKQLYFNLYITVNTMLPRKREVIQSGDDDISFCRALKGETVNT 115
QY 123 AGPVNNEFTIPQGEYQVLE 143
DB 116 TISFSGIKFSKGYKCVVE 136

RESULT 10

US-10-000-066-7
; Sequence 7, Application US/10000066
; Publication No. US20020086364A1
; GENERAL INFORMATION:
; APPLICANT: HONJO, TASUKU
; APPLICANT: KATO, KEIZO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE SAME, AND USE OF THEM
; FILE REFERENCE: Q58771
; CURRENT APPLICATION NUMBER: US/10/000,066
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/529,064
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: PCT/JP98/04515
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: HEI-9-274673
; PRIOR FILING DATE: 1997-10-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-066-7

Query Match 11.8%; Score 101.5; DB 12; Length 160;
Best Local Similarity 24.1%; Pred. No. 0.0015;
Matches 34; Conservative 26; Mismatches 70; Indels 11; Gaps 3;

QY 4 FTATLFLMTLIPSGCGGKAMPYHVCSDSGLEVLVYQSCDPLQ-DGFSVEKSKOL 62
DB 6 FFSFLF--SSIFL-----EAQKYVNCSSDASISYTCDMQYPIISINVPICIELK 55
QY 63 KSNINIRFGILIRREDIKELFDLALMSGSSVNLFSYPCALPKFSFCGRKGEQIY 122
DB 56 GSKGLHIFYPREDLKQLYFNLYITVNTMLPRKREVIQSGDDDISFCRALKGETVNT 115
QY 123 AGPVNNEFTIPQGEYQVLE 143
DB 116 TISFSGIKFSKGYKCVVE 136

RESULT 11

US-09-372-348-26
; Sequence 26, Application US/09372348A
; Publication No. US2003002805A1
; GENERAL INFORMATION:
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Wang, Luquan
; APPLICANT: Zlotnick, Albert
; APPLICANT: Murgolo, Nicholas J.
; APPLICANT: Greene, Jonathan R.
; APPLICANT: Johnston, James A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods

FILE REFERENCE: DX0894K(2d)
CURRENT APPLICATION NUMBER: US/09/372,348A
CURRENT FILING DATE: 1999-08-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 26
LENGTH: 141
TYPE: PRT
ORGANISM: Primate
US-09-372-348-26

Query Match 11.2%; Score 96.5; DB 10; Length 141;
Best Local Similarity 25.6%; Pred. No. 0.0049;
Matches 30; Conservative 20; Mismatches 56; Indels 11; Gaps 3;

QY 33 CSDGLEYVYQSCDPLQ-DGFSVVKCSKQKLSNINIRFGIILREDIKELFLDLALMSQG 91
DB 25 CNSSDAIISYCYCDHLKFPISISSEPCIRLNGTNGFVHEFIPRGNLKYLTFNLF----- 80
QY 92 SVLAFSPY-----ICEALPKFSFCGRKGEQIYAGPVNNPEFTIPQGEYQVLE 143
DB 81 -SVNSTIEHPKXKEVLCGHDDIYSPORALKSETVNTSIPFSFEGILFPKGRVCVAE 136

RESULT 12
US-09-899-917-17
Sequence 17, Application US/09899917
Patent No. US20020119552A1
GENERAL INFORMATION:
APPLICANT: Olsen, Henrik S.
Ruben, Steven M.
TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,917
FILING DATE: 09-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/994,962
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/037,388
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488 0440002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: No. US20020119552A1 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-899-917-17

Query Match 10.9%; Score 94; DB 9; Length 60;
Best Local Similarity 33.3%; Pred. No. 0.003;

Matches 43; Conservative 3; Mismatches 13; Indels 70; Gaps 11;
QY 27 WPTHVVCSDGLEVLYQSCDPLQDPGFSVVKCSKQKLSNINIRFGIILREDIKELFLDLA 86
DB 1 WPTHV-----CLEYSCDP-QDF-FS--CSIRLR-----IKELL----- 29
QY 87 LMSQSSVLFNSYPICEALPKFSFCGRKGEQIYAGPVNNPEFTIPQGEYQVLELYT 146
DB 30 -----GVLSCLKFCG--KGE--YYCP-----IPG-----YL 52
QY 147 EKRSIVACA 155
DB 53 ER--TVACA 59

RESULT 13
US-10-424-599-214951
Sequence 214951, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 214951
LENGTH: 555
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(555)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: clone ID: PAT_MRI3847_36126C.1.pep
US-10-424-599-214951

Query Match 9.5%; Score 81.5; DB 12; Length 555;
Best Local Similarity 25.7%; Pred. No. 1.97
Matches 26; Conservative 18; Mismatches 32; Indels 25; Gaps 4;

QY 48 LODGFSVVKCSKQKLSNINIRFGIILREDIKELFLDLALMSQSSVLFNSYPICEALP 107
DB 66 VQKGYK-DKCYEQIRKVEGRFKNLNLV---FEDL-----KALE 104
QY 108 KFSFCGRKGEQIYAGPVNNPEFTIPQGEYQVLELYT 148
DB 105 EARALGEBLGDVYDVAFCPPRYEI-----FQLMVNYLTER 141

RESULT 14
US-10-424-599-199134
Sequence 199134, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 199134
LENGTH: 170
TYPE: PRT

ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_21842C.1.pap
US-10-424-599-199134

Query Match
Best Local Similarity 21.1%; Score 81; DB 12; Length 170;
Matches 35; Conservative 20; Mismatches 59; Indels 52; Gaps 7;

QY 24 GKAN-PTHVCSDS---GLEVIYQSCDPLQDFGFSYER----- 57
DB 23 GASWVPQVYKVEYKYPGNPLYFCADP-ADYILQIEKYDLDPNPKPGEKLAIRASGP 81
QY 58 ---CSKQKSNINIRGGIILREDIKELFLDLALMSQSSVLPNSFYICEALPKFSFG 113
DB 82 FKEVGGSGSKHGLVKGGLI-----TLINQBRACDTIQADLKP 122
QY 114 RRKGEQIYVAGPVNPEFTIPQGEYQVLELYTEKSTVACANATI 159
DB 123 LKKGELSLTKDVELPR-EIPPGTYVLADVYTEDGDKITCLTAKI 166

RESULT 15
US-10-282-122A-77326

Sequence 77326, Application US/10282122A
Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zykkind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See file wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 77326

LENGTH: 876

TYPE: PRT

ORGANISM: Vibrio cholerae

US-10-282-122A-77326

Best Local Similarity 26.1%; Pred. No. 9;
Matches 37; Conservative 23; Mismatches 40; Indels 42; Gaps 10;

QY 8 LFLWTLIFPSCGGGGKAMPYHV--CSDSGLEVIYQSCDPLQDFGFSYERCKSKQKSN 65
DB 599 IVMNIICTCSPRMGIRTAStGVFLGSGYGLP-----PKERC---KTT 640
QY 66 INI--RGI--LREDIKELFLDLALMSQSSVLPNSFYICEALPKFSFGRRKGEQY 121
DB 641 INLGDEGVINVLEDEVE---TALPRKRC-----PICEIAMDAILDDKSK---LH 687
QY 122 YAGPVNPE---FTIPQGEYQV 140
DB 688 VCG--NNPNCGEFYIEGEPKV 707

Search completed: April 29, 2004, 15:29:31
Job time: 43 secs

Query Match 9.0%; Score 78; DB 12; Length 876;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 29, 2004, 15:21:06 ; Search time 21 seconds
(without alignments)
742.049 Million cell updates/sec

Title: US-09-899-917-2

Perfect score: 862
Sequence: 1 MGCFATLFLWTLIFPSCSG.....ELYTEKSTVACANATIMCS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344	39.9	160	2 S18633	MD-1 protein - chi
2	99	11.5	1137	2 G84581	copla-like retroel
3	81	9.4	406	2 H71139	hypothetical prote
4	79.5	9.2	484	2 H84723	probable triacylgl
5	78	9.0	876	2 B82163	DNA topoisomerase
6	78	9.0	1133	2 S54496	probable membrane
7	77.5	9.0	394	2 A75012	conserved hypothet
8	77.5	9.0	428	2 T14529	S-locus-specific g
9	77	8.9	739	2 AH0393	probable exported
10	77	8.9	739	2 G97400	hypothetical prote
11	76.5	8.9	294	2 T22058	hypothetical prote
12	76.5	8.9	436	2 T28065	hypothetical prote
13	76.5	8.9	452	1 VGBB33	glycoprotein D pre
14	76.5	8.9	471	2 E86192	hypothetical prote
15	75.5	8.8	342	2 D81306	probable UDP-N-ace
16	75.5	8.8	1215	2 C84848	hypothetical prote
17	75.5	8.8	1241	2 F97286	DNA-dependent RNA
18	75.5	8.7	699	2 A96529	hypothetical prote
19	74.5	8.6	484	2 T16595	hypothetical prote
20	73.5	8.5	442	1 VGBERA	glycoprotein D pre
21	73.5	8.5	481	2 E97348	hypothetical prote
22	73	8.5	1106	2 A97819	isoleucine-tRNA 11
23	72	8.4	409	2 E90299	conserved hypochet
24	72	8.4	686	1 D70172	DNA recombinase (r
25	72	8.4	1218	2 S71376	glutamate receptor
26	71.5	8.3	267	2 B90486	ABC transporter, A
27	71.5	8.3	1513	1 RMRZC2	DNA-directed RNA p
28	71	8.2	668	2 S56909	polymyxin B resist
29	71	8.2	887	2 T01113	translation initia

30	71	8.2	1213	2 D66384	unknown protein [i
31	70.5	8.2	218	2 G71875	hypothetical prote
32	70.5	8.2	456	2 H71733	outer membrane pro
33	70.5	8.2	532	2 T49873	calnexin homolog -
34	70.5	8.2	566	1 HM1VD1	hemagglutinin prec
35	70.5	8.2	1474	2 D88550	protein ZC84.6 [im
36	70	8.1	175	1 G69518	isochorismatase (e
37	70	8.1	215	2 P82062	adenylisulfate ki
38	70	8.1	515	2 D84142	1-pyrroline-5-carb
39	70	8.1	794	2 T46073	hypothetical prote
40	70	8.1	950	1 PWBXR1	Ca2+-transporting
41	70	8.1	1116	2 T42213	m-tomoyln, isoform
42	69.5	8.1	440	2 ACO962	D-serine dehydrata
43	69	8.0	316	2 F70441	capsular polysacch
44	69	8.0	385	2 T01332	hypothetical prote
45	69	8.0	591	2 C84220	propionyl-CoA carb

ALIGNMENTS

RESULT 1

S18633 MD-1 protein - chicken

C/Species: Gallus gallus (chicken)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999

A/Accession: S18633; S42854

R/Burk, O.; Klemmner, K.H.

EMBO J. 10, 3713-3719, 1991

A/Title: Estrogen-dependent alterations in differentiation state of myeloid cells caused

A/Reference number: S18633; MUID:92037533; PMID:1718743

A/Accession: S18633

A/Molecule type: mRNA

A/Residues: 1-160 <BUR>

A/Cross-References: EMBL:X60450

R/Burk, O.

submitted to the EMBL Data Library, September 1991

A/Reference number: S42854

A/Accession: S42854

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-130, 'R', 132-160 <BU2>

A/Cross-References: EMBL:X60450; NID:9432637; PID:9432638

C/Superfamily: chicken MD-1 protein

Query Match 39.9%; Score 344; DB 2; Length 160;
Best Local Similarity 45.1%; Pred. No. 2.6e-27;
Matches 60; Conservative 26; Mismatches 47; Indels 0; Gaps 0;

QY	27	WPTHTVCSDSLGLVLYOSCDLPDGFSEVKEKSKQSLKSNINIRFGIIRREDIKELFDLA	86
DB	22	WPTHTVCSDSLGLVLYOSCDLPDGFSEVKEKSKQSLKSNINIRFGIIRREDIKELFDLA	81
QY	87	IMSGSSVLYNFSYPCERAPKPFSCGRKGEQIYAGPVNVPFTTIPGGEYQVLLLELYT	146
DB	82	LIINQKTVLSSETLCPGLSKLIFCGKKGEHLYESPTILGKEIPQGDYITARLTN	141
QY	147	EKRSTVACANATI	159
DB	142	EDRATVACADFTV	154

RESULT 2

G84581 copla-like retroelement pol polyprotein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

A/Accession: G84581

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; McFarr, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Unayam, L.; Tallon, L.C.

ens, D.; Nieman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; NCID:20083487; PMID:10617197
 A:Accession: G84581
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1137 <STO>
 A:Cross-references: GB:AE002093; NID:g3687234; PIDN:AAC62132.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g19840
 A:Map position: 2

Query Match 11.5%; Score 99; DB 2; Length 1137;
 Best Local Similarity 26.3%; Pred. No. 0.13;
 Matches 36; Conservative 23; Mismatches 42; Indels 36; Gaps 7;

QY 10 LMTLIFPSCSG-----GGGKAMPTHTVVCDSGLVLYQSCDPLQDFGFSV--- 55
 DB 448 LMTSAVENFSGGLKRFQGVVYVYQEGGLDR---AKGVFVGY---PVGKGFVWMI 499
 QY 56 --EKCSKQLKSNINIRFGIILREDIKELFLDLALMSGSSVNFSPICGALPKFSPCG 113
 DB 500 EBERCS-----ISNVVFRDV--MYKD--ILNOSTGMSFDPPLATNRIIPSECG 547
 QY 114 RRKGEQIYVAGPVNPE 130
 DB 548 NRKXDEISVQGVSDDD 564

RESULT 3
 H71139
 Hypothetical protein PH0331 - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000
 C:Accession: H71139
 R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohnuki, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Accession: H71139
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-406 <KAM>
 A:Cross-references: GB:AB000002; NID:g3236129; PIDN:BAA29405.1; PID:g3256722
 A:Experimental source: Strain OT3
 A>Note: This accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH0331
 C:Superfamily: conserved hypothetical protein PAB1277

Query Match 9.4%; Score 81; DB 2; Length 406;
 Best Local Similarity 25.8%; Pred. No. 2.6;
 Matches 39; Conservative 27; Mismatches 49; Indels 36; Gaps 9;

QY 1 MKG--FTATLPLMTLIFPSCSGGGGKXA-WPTHTVCSDSGLVLYQSCDPLQDFG--SV 55
 DB 4 MKGASFVTLFLMTLFWSLIFGVPGKLAFLPLLI---MGLLF--DAPGDFEVEREI 56
 QY 56 EKC-----SKQLKSNINIRFGIILREDIKELFLDLALMSGSSVNFSPICGAL 106
 DB 57 EKAQTFVNELEVLVAVRGIGLVAVRENIPKAF---MTSSGSNVGF----- 103
 QY 107 PKFSFGRRKGEQIYVAGPVNPEFTIPOGE 137
 DB 104 --FTYGRSRFQLSYKLLPKRGVYEIPKTE 132

RESULT 4
 H84723
 Probable triacylglycerol lipase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: H84723
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
 Neuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: H84723
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <STO>
 A:Cross-references: GB:AE002093; NID:g4582461; PIDN:AAD24845.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g13690
 A:Map position: 2

Query Match 9.2%; Score 79.5; DB 2; Length 484;
 Best Local Similarity 27.4%; Pred. No. 4.6;
 Matches 34; Conservative 18; Mismatches 43; Indels 29; Gaps 5;

QY 35 DSGLEVLVYQSCDPLQDFGFSYKCSKQLKSNINIRFGIILREDIKELFLDLALMSGSSV 94
 DB 248 ESGFLSLVTSDESKFG--LSCROQLSEIS--RLMKYKGEWSITLAGHSMGSSL 302
 QY 95 LN-FSPYPCGALPK-----PSFGRRRG-----QIYVAGPVNPE 130
 DB 303 AQLLAVIDIAELGLNRRIGKGDIPVTVSFAGPVGNNLFKRCCELVKVRITNVDPV 362
 QY 131 FTIP 134
 DB 363 TKLP 366

RESULT 5
 B82163
 DNA topoisomerase I VC1730 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: B82163
 R:Reidberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
 Chardson, D.; Ermolaeva, M.D.; Vamathevan, U.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P.
 1, R.R.; Mekalanos, J.C.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: AB02035; MUID:20406833; PMID:10952301
 A:Accession: B82163
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-876 <HEI>
 A:Cross-references: GB:AE004251; GB:AE003852; NID:g9656248; PIDN:AAP94880.1; GSPDB:GN00139
 A:Experimental source: serogroup O1, strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC1730
 A:Map position: 1
 C:Superfamily: Dacterial type I DNA topoisomerase

Query Match 9.0%; Score 78; DB 2; Length 876;
 Best Local Similarity 26.1%; Pred. No. 13;
 Matches 37; Conservative 23; Mismatches 40; Indels 42; Gaps 10;

QY 8 LPLMTLIFPSCSGGGGKAMPTHTV--CSDSGLVLYQSCDPLQDFGFSYKCSKQLKSN 65
 DB 599 IVMTNLCTCRPMWIKRSTAGTVLGSGLP-----PKERC---KTT 640
 QY 66 INT--RFGII--LRBDIKELFLDLALMSGSSVNFSPICGALPKFSGCRRRGEOIY 121
 DB 641 INLGDEGVYINLEBVE---TAALRAKRC-----PICETADAVYIIDKRX---LH 687
 QY 122 YAGPVNPE---FTIPOGEYOV 140
 DB 688 VCG--NNPNCGEFTVBSGEFKV 707

RESULT 6
 S54496

probable membrane protein YPR022c - yeast (*Saccharomyces cerevisiae*)

N/Alternate names: hypothetical protein YP9367.02c

C/Species: *Saccharomyces cerevisiae*

C/Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 19-Apr-2002

C/Accession: S54496

R/Baddock, K.; Churcher, C.M.

submitted to the EMBL Data Library, May 1995

A/Reference number: S54059

A/Accession: S54496

A/Molecule type: DNA

A/Residues: 1-1133 <BAD>

A/Cross-references: EMBL:Z49274; NID:g809585; PID:g809587; GSPDB:GN00016; MIPS:YPR022c

A/Experimental source: strain AB972

C/Genetics:

A/Gene: MIPS:YPR022c

A/Cross-references: SGD:S0006226

A/Map position: 16R

C/Keywords: transmembrane protein

F/532-546/Domain: transmembrane #status predicted <TM1>

F/768-784/Domain: transmembrane #status predicted <TM2>

F/931-947/Domain: transmembrane #status predicted <TM3>

F/971-987/Domain: transmembrane #status predicted <TM4>

Query Match 9.0%; Score 78; DB 2; Length 1133;

Best Local Similarity 25.3%; Pred. No. 17;

Matches 37; Conservative 16; Mismatches 31; Indels 62; Gaps 8;

QY 46 DPLADFGFSEKCS-----KQKCS--NINIRFGII--LREDIKE 80

DB 472 DPLATYKIKSKKQCMFSPVPELRYVSIKSIKSLKFMNHPQYGLHPSFHDKQP 531

QY 81 LFLDLALMSQSSVNFYS-----PICNALPKSFGRRRGDEIYYAGPV-----NNP 129

DB 532 ALINLALITGASFLGSEIREQISDPIC-----GPIRLWTFSSHA 570

QY 130 EFTIPQGEYOV-----LLELYTEKRSY 151

DB 571 DQPPSKTYIIQSLLLVEGY-EXTST 595

RESULT 7

A/5012

conserved hypothetical protein PAB1277 - *Pyrococcus abyssi* (strain Orsay)

C/Species: *Pyrococcus abyssi*

C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-2000

C/Accession: A75012

R/Anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A/Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru

A/Reference number: A75001

A/Accession: A75012

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-394 <KAM>

A/Cross-references: GB:AJ248288; GB:AL096836; NID:G5458960; PID:QAB5053.1; PID:G545904

A/Experimental source: strain Orsay

C/Genetics:

A/Gene: PAB1277

C/Superfamily: conserved hypothetical protein PAB1277

Query Match 9.0%; Score 77.5; DB 2; Length 394;

Best Local Similarity 23.4%; Pred. No. 5.7;

Matches 36; Conservative 31; Mismatches 44; Indels 43; Gaps 9;

QY 1 MKG-FTATFLTLIFPSCGGGGA-WPTHVCSDSLAVLYXGCDPLQDFGFSVEK 57

DB 1 MRGVSPFLTIFLWVLSVIFGPKALFPLLIIT---VGMIPDT-----PGGFTVER 51

QY 58 -----CSKQKSNINIRFG-----IIREDIKELFLDLALMSQSSVNF-FTSPICE 103

DB 52 EYTKRVRVVEEYVVKLRVSVKGIIVILKENIIPRAF-----EVKGSATFHFITYGKR 106

QY 104 ALPKPFCGRKGEQIYYAGPVNPEFTIPGE 137

DB 107 EFSFEYSFVPRRG-----EYDIPKTE 128

RESULT 8

T14529

S-locus-specific glycoprotein - wild cabbage (fragment)

N/Alternate names: S glycoprotein

C/Species: *Brassica oleracea* (wild cabbage)

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000

C/Accession: T14529

R/Kusaba, M.; Nishio, T.; Saita, Y.; Hinata, K.; Ockendon, D.

Proc. Natl. Acad. Sci. U.S.A. 94: 7673-7678, 1997

A/Title: Striking sequence similarity in inter- and intra-specific comparisons of class

echinam.

A/Reference number: Z18078; MUID:97352858; PMID:9207151

A/Accession: T14529

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-428 <KUS>

A/Cross-references: EMBL:DS5205; NID:G2351141; PIDN:BA2193.1; PID:G2351142

C/Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology

C/Keywords: glycoprotein

Query Match 9.0%; Score 77.5; DB 2; Length 428;

Best Local Similarity 25.2%; Pred. No. 6.3;

Matches 27; Conservative 20; Mismatches 49; Indels 11; Gaps 4;

QY 49 QDFGFSVEKCSKQKSNINIRFGIILREDIKELFLDLALMSQSSVNFSPICGALPK 108

DB 149 QSFDFPDTLLPEMKQGYNIKTGL-----NRFILAMRNSDDPSGDVSKLENELPE 201

QY 109 FSGGRKRGEOIYYAGPVNPEFT-IPGE-YOVLELYTEKSTVA 153

DB 202 FYLL-KSGFQVHRSGPMNGVRFSIGPENKLSYMYNFTENSEEVA 246

RESULT 9

AH0393

probable exported protein YP03241 [imported] - *Yersinia pestis* (strain CO92)

C/Species: *Yersinia pestis*

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001

C/Accession: AH0393

R/Packhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;

delano-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.; E

11. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, E

Nature 413: 523-527, 2001

A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AH0393

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-246 <KUR>

A/Cross-references: GB:AL590842; PIDN:CAC92476.1; PID:G15981177; GSPDB:GN00175

C/Genetics:

A/Gene: YP03241

C/Superfamily: *Escherichia coli* probable membrane protein yafK

Query Match 8.9%; Score 77; DB 2; Length 246;

Best Local Similarity 29.0%; Pred. No. 3.8;

Matches 31; Conservative 12; Mismatches 30; Indels 34; Gaps 6;

QY 45 CDLPDPPFSVEK-----CSKQKSNI---NIRFGIILREDIKELFLDLALMSQSSVNF 98

DB 13 CLPAASFSSASBPVANSKELKQQLG8SVYIQIFKEERYLELYAKL-----QSEYRLVQS 68

QY 99 YPICAAALPKFSFCG-----FRKGEQIYYAGPVNPEFTIPGGEYOV 140

DB 69 YPIC-----FSGGLGPKRREG-----DFKSPGEGYRI 96

RESULT 10

G96740

hypothetical protein F14023.20 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C/Accession: G96740
 R/Name: A.; Ecker, J.R.; Palm, C.D.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.M.; Chung, M.K.; Corn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: G96740
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-739 <STO>
 A/Cross-references: GB:AE005173, NID:g7239509, PIDN:AAF43235.1, GSPDB:GN00141
 C/Genetics:
 A/Genes: F14023.20
 A/Map position: 1

Query Match 8.9%; Score 77; DB 2; Length 739;
 Best Local Similarity 24.0%; Pred. No. 13;
 Matches 25; Conservative 17; Mismatches 30; Indels 32; Gaps 4;

Qy 48 LQDFGSEKSCQKLSNINIRGILR--EDIKELFLDLALMSGSSVLFSPICPA 104
 Db 264 VQKQKVK-DKCYQIKRAVEDRFRLLTYVFDLK-----A 298

Qy 105 ALPKFSCGRKRGQIYACPVNNPFTIQGXYVLLEYEK 148
 Db 299 ALBARNIGELDIYVAPCFPRYEI---FQLMVLTYER 338

RESULT 11
 T22058
 hypothetical protein F40G12.4 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000
 C/Accession: T22058

R/McMurray, A.
 submitted to the EMBL Data Library, July 1996

A/Reference number: Z19507

A/Accession: T22058

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-294 <WIL>

A/Cross-references: EMBL:Z77661; PIDN:CAE01187.1; GSPDB:GN00023; CESP:F40G12.4

A/Experimental source: clone F40G12

C/Genetics:

A/Genes: CESP:F40G12.4

A/Map position: 5

A/Intons: 59/3; 159/3; 262/1

C/Superfamily: Caenorhabditis elegans hypothetical protein F40G12.4

Query Match 8.9%; Score 76.5; DB 2; Length 294;
 Best Local Similarity 26.7%; Pred. No. 5.2;
 Matches 23; Conservative 13; Mismatches 49; Indels 1; Gaps 1;

Qy 28 PTHVYGDSEGLVLYQSCDPLQD-FGFSVEKSCQKLSNINIRGILRDIKELFLDLA 86
 Db 107 PAHGGSDTYRRLNAQRCDAQKTMWEIKQELRPFKNSTQVLAACREIKECWEDLC 166

Qy 87 LMSGSSVLFSPICPAALPKFSPC 112
 Db 167 FTDSQYERISLAVPELVSHFVVC 192

RESULT 12
 T28066

hypothetical protein ZK867.2 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C/Accession: T28066
 R/Name: M.
 submitted to the EMBL Data Library, November 1995
 A/Description: The sequence of C. elegans cosmid ZK867.
 A/Reference number: Z20464
 A/Accession: T28066
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-436 <NHA>
 A/Cross-references: EMBL:U41039; PIDN:AAA82394.1; CESP:ZK867.2
 C/Genetics:
 A/Genes: CESP:ZK867.2
 A/Intons: 47/3; 79/1; 108/3; 162/1; 212/2; 295/3; 340/3; 367/3

Query Match 8.9%; Score 76.5; DB 2; Length 436;
 Best Local Similarity 21.0%; Pred. No. 8.1;
 Matches 34; Conservative 26; Mismatches 67; Indels 35; Gaps 6;

Qy 33 CSDSGLE-----VLYQSCDPLQDFGFSVEKSCQKLSNINIRGILRDIK 80
 Db 24 CKHGAWEILKMLFRLIGVNTWIDWKKFGQYFGSKXGNWGMIGLQSQLDL 83

Qy 81 LFLDLALMSGSSVLFSPICPAALPKFSPCGRK-----GEOIYAG---- 124
 Db 84 IGLNRIAPREHEVLYFSPYRVEFTISQSPVSRLLIILIAFFISQLYQTDMLAF 143

Qy 125 --PVNNPFTIQGXYVLLEYEKRSVAC-ANATIMCS 162
 Db 144 LSVPLT--YSLPFRSIRKALVHEHOKYIAAFENQTLTCT 182

RESULT 13
 VGBEG3

glycoprotein D precursor - equine herpesvirus 1

C/Species: equine herpesvirus 1

A/Note: host Equus caballus (domestic horse)

C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999

C/Accession: I36802; B36646; PQ0146

R/Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.

submitted to GenBank, March 1992

A/Description: The DNA sequence of equine herpesvirus-1.

A/Reference number: A36805

A/Accession: I36802

A/Molecule type: DNA

A/Residues: 1-452 <TEL>

A/Cross-references: GB:M6664; NID:g330791; PIDN:AA02507.1; PID:g330863

A/Experimental source: strain Ab4P

R/Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.

Virology 189, 304-316, 1992

A/Title: The DNA sequence of equine herpesvirus-1.

A/Reference number: A41831; MUID:92295566; PMID:1338606

A/Contents: annotation; possible protein-coding frames

A/Note: neither amino acid nor nucleotide sequence is given

R/Audomert, J.C.; Winslow, J.; Allen, G.; Paleletti, E.

J. Gen. Virol. 71, 2969-2978, 1990

A/Title: Equine herpesvirus type 1 unique short fragment encodes glycoproteins with homol

A/Reference number: A36646; MUID:91108393; PMID:2177089

A/Accession: B36646

A/Molecule type: DNA

A/Residues: 1-452 <AUD>

A/Cross-references: GB:M6664; NID:g330791; PIDN:AA02507.1; PID:g330863

A/Experimental source: strain Kentucky D

R/Eaton, D.W.; Halliburton, I.W.; Killington, R.A.; Meredith, D.M.; Bonass, W.A.

Gene 101, 201-208, 1991

A/Title: Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine herpesvirus 1

A/Reference number: J00998; MUID:91276272; PMID:1647359

A/Accession: PQ0146

A/Molecule type: DNA

A/Residues: 292-452 <ET>

A/Cross-references: GB:M6299; NID:g330787; PIDN:AAA66546.1; PID:g808672

C/Genetics:
A/Gene: 72
C/Superfamily: herpesvirus glycoprotein D
C/Keywords: glycoprotein; transmembrane protein
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-452/Product: glycoprotein D #status predicted <MAT>
F/399-416/Domain: hydrophobic <HYD>
F/404-422/Domain: transmembrane #status predicted <TM2>
F/103,111,347,396/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/347,396/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.9%; Score 76.5; DB 1; Length 452;
Best Local Similarity 26.6%; Pred. No. 8.9;
Matches 44; Conservative 16; Mismatches 62; Indels 47; Gaps 8;

QY 2 KGFATLFLMTLIPSCSGGGGKAMPHTVYCSDSGLVLYQSCDPLQDFGSVEKSKQ 61
DB 161 KTYSAFL-TWFKIMPTC-----ATPIH-----DVSYMKCKPLSFAMCDE----- 199
QY 62 LKSNINIRGII--LRDIEKELFLDLALMSGSSVL-----NFSYVICA 105
DB 200 -RSDIIMQSLITMAETDDELGLVALAPASASGLYRRVIEDGRRITPTDSVTIPSE 258
QY 106 LP-----KFSFCGRKGEQIYVAGPVNN-----PEFTIPQGEYQVLLDY 145
DB 259 CFIAPQNGNDPDRCTPEQYSGEVFTFRFLGFENFPQGEHMTLKEW 307

RESULT 14

E86192

Hypothetical protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C/Accession: E86192

R/Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurose, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: E86192

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-471 <STO>

A/Cross-references: GB:AEO05172; NID:G6850308; PIDN:AAF29385.1; GSPDB:GN00141

C/Genetics:

A/Map position: 1

Query Match 8.9%; Score 76.5; DB 2; Length 471;
Best Local Similarity 26.6%; Pred. No. 8.9;
Matches 33; Conservative 19; Mismatches 43; Indels 29; Gaps 5;

QY 35 DSGLEVLVYQSCDPLQDFGSVEKSKQKSNINIRFGIILREDIKELFLDLALMSGSSV 94
DB 237 ESGFLGIYTSGESESKRG--LESCREQLLSEIS--RLMKKHGEISITLGHSGSSSL 291
QY 95 LN-FSYVICAALPK-----FSPGGRKGE-----QIYVAGPVNNPE 130
DB 292 AQLIAYDIALGIMQRRDEKPVPTVTFSGPRVGNLGFKKCEBEIGVAKLRITVNDPI 351
QY 131 FTIP 134
DB 352 TKLP 355

RESULT 15

D81306

Probable UDP-N-acetylglucosamine-N-acetyl[muramyl]-(pentapeptide) pyrophosphoryl-undecapate

C/Species: Campylobacter jejuni
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C/Accession: D81306
R/Parhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling,
C.W.; Oball, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrett,
Nature 403, 665-668, 2000
A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A/Reference number: A81550; MUID:20150912; PMID:10688204
A/Accession: D81306
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-342 <PAR>
A/Cross-references: GB:AL139077; GB:AL111168; NID:G6968444; PIDN:CAB73295.1; PID:G696847;
A/Experimental source: serotype O2, strain NCTC 11168
C/Genetics:
A/Gene: murg; Cj1039
C/Superfamily: murg protein
C/Keywords: glycosyltransferase; hexosyltransferase

Query Match 8.8%; Score 75.5; DB 2; Length 342;
Best Local Similarity 25.7%; Pred. No. 7.8;
Matches 37; Conservative 22; Mismatches 34; Indels 51; Gaps 11;

QY 35 DSGLEVLVYQSCDPLQDFGSVEKSKQKSNINIR-----FGIILREDIKELFLDLALMS 89
DB 196 EQNIXIKIHQ-CGK-NDP-----EKCKKHYS-LNIQADIFDPSLLEKMKKN--ADLAISR 246
QY 90 QGSSVLFNSYPICAAAP-----KF-----FSPGGRKGEQIYVAGPVN 127
DB 247 AGASTL--FELCANTLPTIFIPYPAKNGYFNKAFLODQALC-----QIFMGNISIN 297
QY 128 NPEFTIPQGEYQVLLDYTERKT 151
DB 298 LDEF-----FKSITIKLNLNIST 315

Search completed: April 29, 2004, 15:24:22
Job time : 23 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 29, 2004, 15:21:06 ; Search time 17 Seconds

(without alignments)
496.198 Million cell updates/sec

Title: US-09-899-917-2

Perfect score: 862
Sequence: 1 MKGFTALLFLMTLIFPSCSG.....ELYEKSTVACANATIMCS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	862	100.0	162	1 LY86_HUMAN	O95711 homo sapien
2	613	71.1	162	1 LY86_MOUSE	O98188 mus musculus
3	316	39.0	160	1 LY86_CHICK	O90890 gallus galli
4	125	14.5	160	1 LY96_BOVIN	P58754 bos taurus
5	124	14.4	160	1 LY96_CRIGR	P58755 cricetus
6	106	12.3	160	1 LY96_MOUSE	O97159 mus musculus
7	101.5	11.8	160	1 LY96_MOUSE	O97159 mus musculus
8	78	9.0	876	1 TOP1_VIBCH	O9KBD2 vibrio chol
9	77	8.9	205	1 CYSC_VIBPA	O878X6 vibrio para
10	77	8.9	207	1 CYSC_VIBVU	O878X6 vibrio para
11	76.5	8.9	402	1 VGLD_HSVFA	P24872 equine herp
12	76.5	8.9	402	1 VGLD_HSVFA	P24872 equine herp
13	75.5	8.8	342	1 MURG_CAMJE	O9P9Q2 campylobact
14	75.5	8.8	1241	1 RPOB_CLOAB	O97639 clostridium
15	75	8.7	522	1 UAP1_HUMAN	O16222 h udp-n-ace
16	73.5	8.5	442	1 VGLD_HSVFA	P24872 equine herp
17	73.5	8.5	442	1 VGLD_HSVFA	P24872 equine herp
18	72.5	8.4	488	1 YB9E_HUMAN	O98C40 thermomater
19	72	8.4	686	1 RECG_BORBU	O51528 borrelia bu
20	71.5	8.3	214	1 RPOA_EUGVI	O88186 euglena vir
21	71.5	8.3	1513	1 RPOB_OUYSA	P12093 cyria sattiv
22	71	8.2	668	1 PBS2_YRST	P08018 saccharomyc
23	70.5	8.2	532	1 CAX2_ARATH	O38798 arabidopsis
24	70	8.1	215	1 CYSC_VIBCH	O9KBD2 vibrio chol
25	70	8.1	515	1 RPOC_BACHD	O9KBD2 vibrio chol
26	70	8.1	950	1 ATCI_YEAST	P13586 saccharomyc
27	69.5	8.1	440	1 SDHD_SALTY	O82108 salmonella
28	69.5	8.1	440	1 SDHD_SALTY	O82108 salmonella
29	68	8.0	708	1 NICA_MOUSE	P57716 mus musculus
30	68	8.0	7180	1 R1AB_CWUOH	P19751 m replicase
31	68.5	7.9	200	1 RUVA_STIAM	O99E11 staphylococ
32	68.5	7.9	474	1 PPAR_XENLA	P37232 xenopus lae
33	68.5	7.9	1616	1 RRPO_TMOB	P90211 tobamovirus

34	68	7.9	387	1 PEP3_RABIT	P27822 oryctolagus
35	68	7.9	458	1 FK84_HUMAN	O02790 homo sapien
36	68	7.9	708	1 NICA_RAT	O8C9U6 rattus norv
37	68	7.9	849	1 SRK6_BRAOL	O09092 brassica ol
38	67.5	7.8	200	1 RUVA_STAMP	O8C990 staphylococ
39	67.5	7.8	422	1 TRB1_SUITO	O97155 sulfolobus
40	67.5	7.8	434	1 Y610_METUA	O58027 methanococc
41	67.5	7.8	457	1 FK84_RABIT	P27124 oryctolagus
42	67.5	7.8	566	1 HEMA_IADA4	P26562 influenza a
43	67.5	7.8	627	1 K2C1_MOUSE	P04104 mus musculus
44	67	7.8	1422	1 PTPG_CHICK	O98936 gallus gall
45	67	7.8	1914	1 STCK_EMENT	O00706 emeticella

ALIGNMENTS

RESULT 1	ID	LY86_HUMAN	STANDARD	PRT	162 AA.
AC	O95711	O9UCQ4			
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Lymphocyte antigen 86 precursor (MD-1 protein).				
CN	LY86 OR MD1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Monocytes;				
RX	MEDLINE=96436337; PubMed=5763566;				
RA	Miyata Y., Shimazu R., Miyake K., Akashi S., Ogata H., Yamashita Y.,				
RT	Narisawa Y., Kimoto M.;				
RT	"RP105 is associated with MD-1 and transmits an activation signal in				
RT	human B cells.";				
RL	Blood 92:2815-2822(1998).				
RN	[2]				
RP	SEQUENCE OF 45-162 FROM N.A.				
RC	TISSUE=Monocytes;				
RX	MEDLINE=99180501; PubMed=10079183;				
RA	Begum N.A., Tsuji S., Nomura M., Shida K., Azuma I., Hayashi A.,				
RA	Matsunoto M., Seta T., Toyoshima K.;				
RT	"Human MD-1 homologue is a BCG-regulated gene product in monocytes:				
RT	its identification by differential display.";				
RL	Biochem. Biophys. Res. Commun. 256:325-329(1999).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	William S.;				
RA	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Testis;				
RX	MEDLINE=22386257; PubMed=12477932;				
RA	Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Ditachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein W.J., Usdin T.B., Toshiyuki S., Carantini P., Prange C.T.,				
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosch S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huij S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fabry J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman T.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,				
RA	Schreier A., Schein J.E., Jones S.J.M., Maira M.A.;				

Indel

RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: May cooperate with CD180 and TLR4 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS) and cytokine
 CC production. Important for efficient CD180 cell surface expression
 CC (by similarity).
 CC SUBUNIT: Binds CD180.
 CC -1- SUBCELLULAR LOCATION: Extracellular; associated with CD180 at the
 CC cell surface.
 CC -1- TISSUE SPECIFICITY: Highly expressed in B-cells, monocytes and
 CC tonsil.
 CC -1- INDUCTION: In monocytes, down-regulated by the cell-wall fraction
 CC of Mycobacterium bovis (BCG-CMS).
 CC -----
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL, AF057178; AAC98152.2; -;
 DR EMBL, AB020499; BAA76410.1; ALT_INT.
 DR EMBL, AL031123; CAB76262.1; -;
 DR EMBL, BC038846; AAH38846.1; -;
 DR Genew: HGNC:16837; LY86.
 DR MIM: 605241; -;
 DR GO, GO:0005886; C:plasma membrane; TAS.
 DR GO, GO:0006915; P:apoptosis; TAS.
 DR GO, GO:0008283; P:cell proliferation; TAS.
 DR GO, GO:0006959; P:humoral immune response; TAS.
 DR InterPro: IPR003172; E1_DerP2_DerF2.
 DR InterPro: IPR007110; I9-1ike.
 DR Pfam: PF02221; E1_DerP2_DerF2; 1.
 DR SMART: SM00737; ML; 1.
 DR KX Immune response; Inflammatory response; Signal; Polymorphism.
 DR FM SIGNAL 1 20 POTENTIAL.
 DR CHAIN 21 162 LYMPHOCYTE ANTIGEN 86.
 FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 160 160 M -> V (in dbSNP:1802323).
 FT /FTId=VAR_014539.
 FT SEQUENCE 162 AA; 17905 MW; 3B6497E2DB4C6F27 CRC64;
 SQ
 Query Match 100.0%; Score 862; DB 1; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-82;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKGFTALFLMTLTPSCSGGGGKAMPYVVCSDGLFVLYOSCDPLQDFGFSVKKCK 60
 Db 1 MKGFTALFLMTLTPSCSGGGGKAMPYVVCSDGLFVLYOSCDPLQDFGFSVKKCK 60
 QY 61 QLKSNINIRFGIILREDIKELFLDLALMSOGSSVLYNFSPICEAALPKFSFGRRKGEQI 120
 Db 61 QLKSNINIRFGIILREDIKELFLDLALMSOGSSVLYNFSPICEAALPKFSFGRRKGEQI 120
 QY 121 YYAGPVNNPEFTIPQGEYQVLIETEKRSIVACANATIMCS 162
 Db 121 YYAGPVNNPEFTIPQGEYQVLIETEKRSIVACANATIMCS 162

RESULT 2
 LY86_MOUSE
 ID LY86_MOUSE STANDARD; PRT; 162 AA.
 AC 088188;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lymphocyte antigen 86 precursor (MD-1 protein).
 GN LY86 OR MD1.
 OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murine; Mus.
 CC NCB1_TaxId=10090;
 RN (1)
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 20-44.
 RP TISSUE=B-cell;
 RX MEDLINE=98349386; PubMed=9686597;
 RA Miyake K., Shimazu R., Kondo J., Niki T., Akashi S., Ogata H.,
 RA Yamashita Y., Miura Y., Kimoto M.;
 RT "Mouse MD-1, a molecule that is physically associated with RPI05 and
 RT positively regulates its expression.";
 RL J. Immunol. 161:1348-1353(1998).
 RL [2]
 RP FUNCTION.
 RX MEDLINE=20384784; PubMed=10925274;
 RA Gorczynski R.M., Chen Z., Clark D.A., Hu J., Yu G., Li X., Tsang W.,
 RA Haddad S.;
 RT "Regulation of gene expression of murine MD-1 regulates subsequent T
 RT cell activation and cytokine production.";
 RL J. Immunol. 165:1925-1932(2000).
 CC -1- FUNCTION: May cooperate with CD180 and TLR4 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS) and cytokine
 CC production. Important for efficient CD180 cell surface expression.
 CC -1- SUBUNIT: Binds CD180.
 CC -1- SUBCELLULAR LOCATION: Extracellular; associated with CD180 at the
 CC cell surface.
 CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, liver, brain and
 CC thymus, and at lower levels in kidney.
 CC -----
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL, AB007599; BAA32399.1; -;
 DR MGD, MGI:1321404; LY86.
 DR InterPro: IPR003172; E1_DerP2_DerF2.
 DR InterPro: IPR007110; I9-1ike.
 DR Pfam, PF02221; E1_DerP2_DerF2; 1.
 DR SMART: SM00737; ML; 1.
 DR KX Immune response; Inflammatory response; Signal.
 DR FM SIGNAL 1 19
 DR CHAIN 20 162 LYMPHOCYTE ANTIGEN 86.
 FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 162 AA; 17811 MW; EED25DEA64A372E CRC64;
 SQ
 Query Match 71.1%; Score 613; DB 1; Length 162;
 Best Local Similarity 66.7%; Pred. No. 1.5e-56;
 Matches 108; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 1 MKGFTALFLMTLTPSCSGGGGKAMPYVVCSDGLFVLYOSCDPLQDFGFSVKKCK 60
 Db 1 MKGFTALFLMTLTPSCSGGGGKAMPYVVCSDGLFVLYOSCDPLQDFGFSVKKCK 60
 QY 61 QLKSNINIRFGIILREDIKELFLDLALMSOGSSVLYNFSPICEAALPKFSFGRRKGEQI 120
 Db 61 QLKSNINIRFGIILREDIKELFLDLALMSOGSSVLYNFSPICEAALPKFSFGRRKGEQI 120
 QY 121 YYAGPVNNPEFTIPQGEYQVLIETEKRSIVACANATIMCS 162
 Db 121 YYAGPVNNPEFTIPQGEYQVLIETEKRSIVACANATIMCS 162

RESULT 3
 LY86_CHICK
 ID LY86_CHICK STANDARD; PRT; 160 AA.
 AC 090890;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lymphocyte antigen 86 precursor (MD-1 protein).
GN LY86 OR MD1.
OS Gallus gallus (Chicken).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=9203753; PubMed=1718743;
RA Burk O., Klempner K.-H.;
RT "Estrogen-dependent alterations in differentiation state of myeloid cells caused by a v-myb/estrogen receptor fusion protein.";
RL EMO J. 10:3713-3719(1991).
CC - FUNCTION: May cooperate with CD180 and TLR4 to mediate the innate immune response to bacterial lipopolysaccharide (LPS) and cytokine production. Important for efficient CD180 cell surface expression (By similarity).
CC - SUBUNIT: Binds CD180 (By similarity).
CC -1- SUBCELLULAR LOCATION: Extracellular; associated with CD180 at the cell surface (By similarity).
CC -1- TISSUE SPECIFICITY: Detected in the macrophage-like 10.4 cells.
CC -1- INDUCTION: By myd.
CC -----
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CC -----
DR EMBL: X60450; CAA42980.1; -
DR PIR: S18633; S18633.
DR InterPro: IPR003172; E1_Derp2_Derp2.
DR InterPro: IPR007110; I9_1like.
DR Pfam: PF02221; E1_Derp2_Derp2; 1.
DR SMART: SM00737; ML; 1.
KM Immune response; Inflammatory response; Signal.
FT SIGNAL: 1 20
FT CHAIN: 21 160 LYMPHOCYTE ANTIGEN 86.
FT SEQUENCE: 160 AA; 18114 MW; 6E3345141E33C007 CRC64;
SQ
Query Match 39.0%; Score 336; DB 1; Length 160;
Best Local Similarity 44.4%; Pred. No. 9.3e-28;
Matches 59; Conservative 26; Mismatches 48; Indels 0; Gaps 0;

CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
CX NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RA Guionaud C.T., Dubey C., Zunker J.R., Sonstegard T.S., Jung T.W.;
RT "Role of bovine TLR2, TLR4 and CD14 in the recognition of bacterial constituents";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cooperates with TLR4 in the innate immune response to bacterial lipopolysaccharide (LPS), and with TLR2 in the response to cell wall components from Gram-positive and Gram-negative bacteria. Enhances TLR4-dependent activation of NF-kappa-B. Cells expressing both MD2 and TLR4, but not TLR4 alone, respond to LPS (By similarity).
CC -1- SUBUNIT: Heterogeneous homopolymer formed from homodimers; disulfide-linked. Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TLR4. Binds to the extracellular domains of TLR2 and TLR4 (By similarity).
CC -1- SUBCELLULAR LOCATION: Extracellular (By similarity).
CC -----
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CC -----
DR EMBL: AF368418; AAL16721.1; -
DR InterPro: IPR003172; E1_Derp2_Derp2.
DR InterPro: IPR007110; I9_1like.
DR Pfam: PF02221; E1_Derp2_Derp2; 1.
DR SMART: SM00737; ML; 1.
KM Immune response; Inflammatory response; Signal; Glycoprotein.
FT SIGNAL: 1 16
FT CHAIN: 17 160 LYMPHOCYTE ANTIGEN 96.
FT DISULFID: 95 105 BY SIMILARITY.
FT CARBOHYD: 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD: 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD: 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE: 160 AA; 18483 MW; D97605E5E9B352 CRC64;
SQ
Query Match 14.5%; Score 125; DB 1; Length 160;
Best Local Similarity 25.6%; Pred. No. 8e-06;
Matches 41; Conservative 29; Mismatches 70; Indels 20; Gaps 7;

RESULT 4
LY96_BOVIN
ID LY96_BOVIN STANDARD; PRT; 160 AA.
AC P58754;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lymphocyte antigen 96 precursor (MD-2 protein).
GN LY96 OR MD2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT 5
LY96_CRIGR
ID LY96_CRIGR STANDARD; PRT; 160 AA.
AC P58755;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lymphocyte antigen 96 precursor (MD-2 protein).
GN LY96 OR MD2.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia;Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
CC Cricetus.
CC NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT TYR-95.
RC TISSUE=Ovarian carcinoma;
RX MEDLINE=21329172; PubMed=1435474;
RA Schromm A.B., Lien E., Henneke P., Chow J.C., Yoshimura A., Heine H.,
Latz E., Munk B.G., Schwartz D.A., Miyake K., Golenbock D.T.;
RT "Molecular genetic analysis of an endotoxin nonresponder mutant cell
line. A point mutation in a conserved region of MD-2 abolishes
RT endotoxin-induced signaling."
RL J. Exp. Med. 194:79-88(2001).
CC -1- FUNCTION: Cooperates with TLR4 in the innate immune response to
bacterial lipopolysaccharide (LPS), and with TLR2 in the response
to cell wall components from Gram-positive and Gram-negative
bacteria. Enhances TLR4-dependent activation of NF-kappa-B. Cells
expressing both MD2 and TLR4, but not TLR4 alone, respond to LPS
(By similarity).
CC -1- SUBUNIT: Heterogeneous homopolymer formed from homodimers;
disulfide-linked. Belongs to the lipopolysaccharide (LPS)
receptor, a multi-protein complex containing at least CD14, LY96
and TLR4. Binds to the extracellular domains of TLR2 and TLR4 (By
similarity).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC
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CC
CC EMBL; AF325501; AAK57984.1; -
DR InterPro; IPR003172; EI_Derp2_Derp2.
DR InterPro; IPR007110; I9-1like.
DR Pfam; PF02221; EI_Derp2_Derp2; 1.
DR SMART; SM00737; ML; 1.
KW Immune response; Inflammatory response; Signal; Glycoprotein;
KW Polymorphism.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 160 LYMPHOCYTE ANTIGEN 96.
FT DISULFID 95 105 BY SIMILARITY.
FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 95 95 C -> Y (IN ENDOTOXIN NONRESPONDER).
SQ SEQUENCE 160 AA; 18357 MW; 0E533B1A5B46DD6 CRC64;
Query Match 14.4%; Score 124; DB 1; Length 160;
Best Local Similarity 25.4%; Pred. No. 1e-05; 72; Indels 2; Gaps 2
Matches 33; Conservative 23; Mismatches
QY 33 CSDGLELYVQSCDPLQ-DFGFSVVKCSKQSLNSININFGILTRDIELFUDALMSQG 91
DB 25 CNSSDPTATSYSCDSMKPFPSITAPCITLTKGTNGFLHKIFPRDRLKLYFNLSINNS 84
QY 92 SSVYNFSPVPCGAAALPKFSFGCGRRRGEQIYVAGPVNNPFITLPOGEYQVLE-LTXEKS 150
DB 85 IEVPRKRETHICGYDNNYSFCALNGEIVNIVVPSFKGILPFGQYRCVAALVGDNE 144
QY 151 TVACANATIM 160
DB 145 KLFCINFTII 154
LY96_MOUSE
ID LY96_MOUSE STANDARD; PRT; 160 AA.
AC Q9UHF9;
DT 28-FEB-2003 (rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, last sequence update)
 DT 10-OCT-2003 (Rel. 42, last annotation update)
 DE Lymphocyte antigen 96 precursor (MD-2 protein) (ESOP-1).
 GN LY96 OR MD2 OR ESOP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20352025; PubMed=10891475;
 RX Kato K., Morrison A.M., Nakano T., Tashiro K., Honjo T.;
 RA "ESOP-1, a secreted protein expressed in the hematopoietic, nervous,
 RT and reproductive systems of embryonic and adult mice."
 RL Blood 96:362-364 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=20191999; PubMed=10725698;
 RA Akashi S., Shimazu R., Ogata H., Nagai Y., Takeda K., Kimoto M.,
 RA Miyake K.;
 RT "Cell surface expression and lipopolysaccharide signaling via the Toll-
 RT like receptor 4-MD-2 complex on mouse peritoneal macrophages."
 RL J. Immunol. 164:3471-3475 (2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=1085560; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Komio H., Adachi J., Fukuda S.,
 RA Aizawa K., Iizawa M., Nishi K., Kiyasawa H., Kondo S., Yamataka I.,
 RA Saito T., Ozakura Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochua H.,
 RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Struhl P., Suzuki R., Tomita M., Wagner L., Watanabe T.,
 RA Sakai K., Oikido T., Furuno M., Anon H., Baldarelli R., Barh G.,
 RA Blake J., Boileau D., Botunga N., Carrini P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690 (2001).
 CC -1- FUNCTION: Cooperates with TLR4 in the innate immune response to
 CC bacterial lipopolysaccharide (LPS), and with TLR2 in the response
 CC to cell wall components from Gram-positive and Gram-negative
 CC bacteria. Enhances TLR4-dependent activation of NF-kappa-B. Cells
 CC expressing both MD2 and TLR4, but not TLR4 alone, respond to LPS
 CC (by similarity).
 CC -1- SUBUNIT: Heterogeneous homopolymer formed from homodimers;
 CC disulfide-linked. Belongs to the lipopolysaccharide (LPS)
 CC receptor, a multi-protein complex containing at least CD14, LY96
 CC and TLR4. Binds to the extracellular domains of TLR2 and TLR4 (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, bone marrow,
 CC thymus, liver, kidney, ovary and decidua. Detected at lower levels
 CC in testis, small intestine and skin.
 CC -----
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 CC -----
 OR EMBL; AF168120; AAF89634.1; -

DR EMBL; AB018550; BAA93619.1; -
DR EMBL; AK019283; BAB31645.1; -
DR MGD; MGI:1341909; LY96.
DR InterPro; IPR003172; E1_Derp2_Derp2.
DR InterPro; IPR007110; Ig_Like.
DR Pfam; PF02221; E1_Derp2_Derp2; 1.
DR SMART; SM00737; MD; 1.
KW Immune response; Inflammatory response; Signal; Glycoprotein.
FT SIGNAL 1 18
FT CHAIN 19 160
FT DISULFID 95 105
FT CARBOHYD 26 105
FT CARBOHYD 114 114
FT CARBOHYD 150 150
SQ SEQUENCE 160 AA; 18394 MW; E224D17E5D5429E2 CRC64;
Query Match 12.3%; Score 106; DB 1; Length 160;
Best Local Similarity 26.3%; Pred. No. 0.00076;
Matches 36; Conservative 24; Mismatches 61; Indels 16; Gaps 5;
QY 33 GSDGLEVLVYQSCDPLQ-DFGFSVEKSKQLKSNINIRFGIILREDIKELFDLALMSQG 91
DB 25 CNSSDALISYSCDHLKFPISISSEPCILRGTNGFVHVEFIPRGNLKLXLYENLFI---- 80
QY 92 SSVLNFSYP-----ICEALPKPFCGRKRGEOIYAGPVNNEPTIPQGEQVLELEY- 145
DB 81 -SYNSELPRKEVLCGHDDDSFCRALKGETVNTSTFSEGLIFPKGHKCYAEKIA 139
QY 146 --TEKRSTVACANATIM 160
DB 140 GDTSEK-LFCINFTII 154
RESULT 7
LY96 HUMAN STANDARD; PRT; 160 AA.
AC Q9Y6Y9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lymphocyte antigen 96 precursor (MD-2 protein) (ESOP-1).
GN LY96 OR MD2 OR ESOP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus; PubMed=10359581;
RX MEDLINE=99288036; PubMed=10359581;
RA Shimazu R., Akashi S., Ogata H., Nagai Y., Fukudome K., Miyake K.,
RA Kimoto M.,
RT "MD-2, a molecule that confers lipopolysaccharide responsiveness on
RT Toll-like receptor 4";
RL J. Exp. Med. 189:1777-1782 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20352025; PubMed=10891475;
RA Kato K., Morrison A.M., Nakano T., Tashiro K., Honjo T.,
RT "ESOP-1, a secreted protein expressed in the hematopoietic, nervous,
RT and reproductive systems of embryonic and adult mice";
RL Blood 96:362-364 (2000).
RN [3]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF CYS-95.
RX MEDLINE=21329172; PubMed=11435474;
RA Letz E., Monks B.G., Schwartz D.A., Miyake K., Golensbock D.T.,
RT "Molecular genetic analysis of an endotoxin nonresponder mutant cell
RT line: A point mutation in a conserved region of MD-2 abolishes
RT endotoxin-induced signaling";
RL J. Exp. Med. 194:79-88 (2001).
RN [4]
RP SEQUENCE FROM N.A.

RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA DiCicco L., Marusha K., Farmer A.F., Rubin G.M., Hong J.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cassavatt T.L., Schetz T.B.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey U., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Boufield G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP INTERACTION WITH TLR2 AND TLR4.
RX MEDLINE=21103214; PubMed=11160242;
RA Dzarakaki R., Wang Q., Miyake K., Kirschning C.J., Gupta D.,
RT "MD-2 enables Toll-like receptor 2 (TLR2)-mediated responses to
RT lipopolysaccharide and enhances TLR2-mediated responses to
RT Gram-positive and Gram-negative bacteria and their cell wall
RT components";
RL J. Immunol. 166:1938-1944 (2001).
RN [6]
RP DISULFIDE-BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=21477444; PubMed=11593030;
RA Vincent A., Mazzoni A., Spitzer J.A., Segal D.M.;
RT "Secreted MD-2 is a large polymeric protein that efficiently confers
RT lipopolysaccharide sensitivity to Toll-like receptor 4";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12156-12161 (2001).
RN [7]
RP INTERCHAIN DISULFIDE BOND.
RX MEDLINE=22558532; PubMed=12642668;
RA Mullen G.E.D., Kennedy M.N., Vincent A., Mazzoni A., Leifer C.A.,
RA Davies D.R., Segal D.M.;
RT "The role of disulfide bonds in the assembly and function of MD-2";
RL Proc. Natl. Acad. Sci. U.S.A. 100:3919-3924 (2003).
CC -!- FUNCTION: Cooperates with TLR4 in the innate immune response to
CC bacterial lipopolysaccharide (LPS), and with TLR2 in the response
CC to cell wall components from Gram-positive and Gram-negative
CC bacteria. Enhances TLR4-dependent activation of NF-kappa-B. Cells
CC expressing both MD2 and TLR4, but not TLR4 alone, respond to LPS.
CC -!- SUBUNIT: Heterogeneous homopolymer formed from homodimers;
CC disulfide-linked. Belongs to the lipopolysaccharide (LPS)
CC receptor, a multi-protein complex containing at least CD14, LY96
CC and TLR4. Binds to the extracellular domains of TLR2 and TLR4.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- PTM: N-glycosylated; high-mannose.
CC
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CC
CC EMBL; AB018549; BAA78717.1; -
CC EMBL; AF168121; AAP89635.1; -
CC EMBL; BC020690; AAH20690.1; -
CC Genew; HGNC:17156; LY96.
CC MIM; 605243; -
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0015026; F:coreceptor activity; TAS.
DR GO; GO:0006961; P:antibacterial humoral response (sensu Inver. . .; TAS.

DR GO: GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 DR GO: GO:0006968; P:cellular defense response; TAS.
 DR InterPro: IPR003172; E1_Derp2_Derp2.
 DR InterPro: IPR007110; Ig_Like.
 DR Pfam: PF02221; E1_Derp2_Derp2; 1.
 DR SMART: SM00737; Mf_1.
 KW Immune response; inflammatory response; Signal; Glycoprotein.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 160 LYMPHOCYTE ANTIGEN 96.
 FT DISULFID 95 105 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 114 114 C-Y: ABOLISHES LPS-RESPONSE.
 FT MUTAGEN 95 95
 SQ SEQUENCE 160 AA; 18446 MW; 1E83AF583636D7A CRC64;

Query Match 11.8%; Score 101.5; DB 1; Length 160;
 Best Local Similarity 24.1%; Pred. No. 0.0022;
 Matches 34; Conservative 26; Mismatches 70; Indels 11; Gaps 3;

QY 4 FTATPLMTLIPSCSGGGGKAMPHTVVCSDGLEVLVYOSCDPLQ-DGFSYEKSKQL 62
 DB 6 FFSITL--SSIF-----EAKQYWCNSSDASISTYCDKQYPIISINVPICELK 55
 QY 63 KSNINIRFGIILREDIKELFLDLALMSQSSVNFSPICEALPRFSYCGRRKGEQIVY 122
 DB 56 GSKGLHIFIPRBDLKOYFNLYITMNTNLPRKEVICRGSDDDYSCRLMKGETVNT 115
 QY 123 AGPVNPEFTIPQGEYGVLE 143
 DB 116 TISFSEKIKFSKQKXCVVE 136

RESULT 8
 TOP1_VIBCH STANDARD; PRT; 876 AA.
 ID TOP1_VIBCH
 AC Q9KR82;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
 DE (unwinding enzyme) (Swivelase).
 GN TOPA OR VC1730.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OC NCBI_Taxid=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; Pubmed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dasol I., Sellers P.,
 RA McDonald L., Uffereback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.W.;
 RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae.";
 RT Nature 406:477-483 (2000).
 RL Nature 406:477-483 (2000).
 CC -1- FUNCTION: The reaction catalyzed by topoisomerases leads to the
 CC conversion of one topological isomer of DNA to another.
 CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
 CC DNA, followed by passage and rejoining.
 CC -1- SUBUNIT: Monomer (by similarity).
 CC -1- MISCELLANEOUS: When a topoisomerase transiently breaks a DNA
 CC backbone bond, it simultaneously forms a protein-DNA link, in
 CC which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus
 CC at one end of the enzyme-severed DNA strand.
 CC -1- SIMILARITY: Belongs to the prokaryotic type I/III topoisomerase
 CC family.
 CC -----
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DR EMBL: AE004251; AAF94880.1; -.
 DR PIR: B82163; B82163.
 DR HSSP: P06612; 1ECL.
 DR TIGR: VC1730; -.
 DR InterPro: IPR005733; DNA_top1_bact.
 DR InterPro: IPR000380; DNA_topoisomerase.
 DR InterPro: IPR003601; DNATop1_ATP_bind.
 DR InterPro: IPR003602; DNATop1_DNA_bind.
 DR InterPro: IPR006171; Toprim_dom.
 DR InterPro: IPR006154; Toprim_sub.
 DR Pfam: PF01131; Topoisom_bact; 1.
 DR Pfam: PF01751; Toprim; 1.
 DR Pfam: PF01396; ZFC4_Topoisom; 2.
 DR PRINTS: PR00417; PRTISRAS31.
 DR SMART: SM00437; TOP1AC; 1.
 DR SMART: SM00436; TOP1BC; 1.
 DR SMART: SM00493; TOP1RM; 1.
 DR TIGRFAMS: TIGR01051; topa_bact; 1.
 DR PROSITE: PS00396; TOPOISOMERASE_I_PROK; 1.
 KW Isomerase; Topoisomerase; DNA-binding; Zinc-finger; Metal-binding;
 KW Repeat; Complete proteome.
 FT ZN_FING 668 695 C4-TYPE 1.
 FT ZN_FING 717 742 C4-TYPE 2.
 FT ACT_SITE 327 327 DNA_CLEAVAGE (BY SIMILARITY).
 SQ SEQUENCE 876 AA; 97909 MW; 8A5BC9148CA1B753 CRC64;

Query Match 9.0%; Score 78; DB 1; Length 876;
 Best Local Similarity 26.1%; Pred. No. 4.9;
 Matches 37; Conservative 23; Mismatches 40; Indels 42; Gaps 10;

QY 8 LFWLTLIPSCSGGGGKAMPHTVVCSDGLEVLVYOSCDPLQDGFSEYKSKQLKSN 65
 DB 599 IVMNMLGPTCSRPMGIRTAISTGVFLGSGYGLP-----PRERC-----KIT 640
 QY 66 INT--RFGIT--LREDIKELFLDLALMSQSSVNFSPICEALPRFSYCGRRKGEQIV 121
 DB 641 INLGESEVINVLDEVE---TAALRAKRC-----PICEYMDAYLIDDKK--LH 687
 QY 122 YAGPVNPE---FTIPQGEYGV 140
 DB 688 VCG--NNPNCGRGFTVEGEFVKV 707

RESULT 9
 CYSC_VIBPA STANDARD; PRT; 205 AA.
 ID CYSC_VIBPA
 AC Q97SX6;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adenylsulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-
 DE 5-phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-
 DE phosphotransferase).
 GN CYSC OR VP0296.
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OC NCBI_Taxid=670;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RIMD 2210633 / Serotype O3:K6;
 RX MEDLINE=22508454; Pubmed=1620739;
 RA Makino K., Oshita K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Najima M., Nakano M., Yamaehita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RA "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

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RT distinct from that of V. cholerae."
RL Lancel 361743-749(2003).
CC -1- FUNCTION: Catalyzes the synthesis of activated sulfate.
CC -1- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
CC phosphoadenylylsulfate.
CC -1- PATHWAY: Sulfate activation; cysteine biosynthesis reductive
CC branch, second step.
CC -1- SIMILARITY: Belongs to the APS kinase family.
CC
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CC
CC EMBL; AF005073; BAC58559.1; -.
DR HAMAP; MF_00065; -.
DR InterPro; IPR002891; APS_kinase.
DR Pfam; PF01583; APS_kinase; 1.
KW Transferase; kinase; Cysteine biosynthesis; ATP-binding;
KW phosphorylation; Complete proteome.
FT NP BIND 39 46 ATP (BY SIMILARITY).
FT ACT_SITE 113 113 PHOSPHOSERINE INTERMEDIATE (BY
FT SIMILARITY).
SQ SEQUENCE 205 AA; 22894 MW; 03696F141F48199F CRC64;

Query Match 8.9%; Score 77; DB 1; Length 205;
Best Local Similarity 26.3%; Pred. No. 1.1;
Matches 50; Conservative 20; Mismatches 56; Indels 64; Gaps 14;

QY 2 KGETATL-----FLMTLIFPSCGGGGGK-----AMPTHVVCSDSGLEVLQ 43
DB 21 KQRAELKKQKPAVLW---FTGLSGAGKSTVAGALENRLAEQGYHYLLDGN---VRHG 74
QY 44 SCDFLODFGVSVCCKQKLSNINIRFG-----ILIREDI-----KELFLDLA 86
DB 75 LC---SDLGFS---EQDRRENIR-RIGELAKIMADAGLIVTAFTSPHRAERQLVRD-- 124
QY 87 LMSQGSVV---LNFSPICEALPKFSCGRKKE-----QIYAGPVNNEFTIPQG 136
DB 125 LPEGFPIEFVVAASLEVCGRDPKGLYKARAGELPNFTGIDSEYQAPI-NPEIDLPAG 183
QY 137 EYQV--LLEL 144
DB 184 EKSEVELEVL 193

RESULT 10
CYSC_VIBVU STANDARD; PRT; 207 AA.
ID CYSC_VIBVU
AC 08DE75;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adenylylsulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-
DE 5-phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-
DE phosphotransferase).
GN CYSC OR VV10723.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CWCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CWCP6."
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the synthesis of activated sulfate.
CC -1- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-

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CC phosphoadenylylsulfate.
CC -1- PATHWAY: Sulfate activation; cysteine biosynthesis reductive
CC branch, second step.
CC -1- SIMILARITY: Belongs to the APS kinase family.
CC
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CC
CC EMBL; AE016799; AAC09232.1; -.
DR HAMAP; MF_00065; -.
DR InterPro; IPR002891; APS_kinase.
DR Pfam; PF01583; APS_kinase; 1.
DR ProDom; PD002350; APS_kinase; 1.
DR TIGRFAMs; TIGR00455; apsk; 1.
KW Transferase; kinase; Cysteine biosynthesis; ATP-binding;
KW phosphorylation; Complete proteome.
FT NP BIND 39 46 ATP (BY SIMILARITY).
FT ACT_SITE 113 113 PHOSPHOSERINE INTERMEDIATE
FT (BY SIMILARITY).
SQ SEQUENCE 207 AA; 22886 MW; 225B1E471193951B CRC64;

Query Match 8.9%; Score 77; DB 1; Length 207;
Best Local Similarity 25.0%; Pred. No. 1.1;
Matches 45; Conservative 26; Mismatches 51; Indels 58; Gaps 13;

QY 10 LMTLIFPSCGGG-----GKAMPTHVVCSDSGLEVLQSCDPLQDFGSEYK 57
DB 35 LW---FTGLSGAGKSTVAGALENRLAEQGYHYLLDGN---VRHGIC---SDLGFS--- 82
QY 58 CSKOLKSNINIRFG-----ILIREDI-----KELFLDLALMSQGSVV---LNF 97
DB 83 -TQDRRENIR-RIGELAKIMADAGLIVTAFTSPHRAERQLVRD--LPEGFPIEFV 138
QY 98 SYPICEALPKFSCGRKKEQIYAG-----PVNNEFTIPQGE--QVLLLEYLTK 148
DB 139 SLEVCGRDPKGLYKARAGELPNFTGIDSEYVFL-NPEIDLPAGKGLIEALVDLVEQ 197

RESULT 11
VGLD_HSVEA STANDARD; PRT; 402 AA.
ID VGLD_HSVEA
AC P24872;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-AUG-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glycoprotein D precursor (Glycoprotein 17/18).
GN GD OR GP17/18 OR 72.
OS Equine herpesvirus type 1 (strain AB1) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10328;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92268882; PubMed=1316942;
RA Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,
RA Bonas W.A.;
RT "Identification of the equine herpesvirus type 1 glycoprotein 17/18
RT as a homologue of herpes simplex virus glycoprotein D."
RT J. Gen. Virol. 73:1227-1233(1992).
RN [2]
RP SEQUENCE OF 242-402 FROM N.A.
RA MEDLINE=91276722; PubMed=1647359;
RA Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,
RA Bonas W.A.;
RT "Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine
RT herpesvirus type-1 short unique region."
RT J. Gen. Virol. 72:203-208(1991).
CC -1- SIMILARITY: Belongs to the herpesviruses glycoprotein D family.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M36299; AAA46087.1; -.
CC DR InterPro: IPR002896; Herpes_glycop_D.
CC DR InterPro: IPR007110; Ig-like.
CC Pfam: PF01537; Herpes_glycop_D; 1.
CC Glycoprotein; Transmembrane; Signal.
CC SIGNAL 1 30 POTENTIAL.
CC CHAIN 31 402 GLYCOPROTEIN D.
CC DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 356 372 POTENTIAL.
CC DOMAIN 373 402 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 402 AA; 45211 MW; 78A059323D0238C CRC64;

Query Match 8.9%; Score 76.5; DB 1; Length 402;
Best Local Similarity 26.0%; Pred. No. 2.7;
Matches 44; Conservative 16; Mismatches 62; Indels 47; Gaps 8;

QY 2 KGTATLFLMTLIPSCSGGGGKAMPYHVCSDSLGVLYGSCDPLQDFGSVEKSKQ 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 111 KTSARL-TWFKIMPTC-----ATPIH-----DVSVMKCNPKLSFAMCDE----- 149
QY 62 LKSNINIRFGII--LRDIKELFLDLALMSGSSVL-----NFSYPICEAA 105
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 150 -RSDILMQASLTMAAETDDELGLVLAAPASASGLRYRIETIDGRQIYTDTSVTIPSER 208
QY 106 LP-----KFSFGGRKGEQIYVAGPVNN---PEFTIPQGEYVLTLELY 145
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 209 CPIAFEQNGNPDRCKTPEQYSRGEVFTRRFLGSEFNPQGEHMTWLKFW 257

RESULT 12
VGID_HSVB STANDARD; PRT; 452 AA.
ID VGID_HSVB STANDARD; PRT; 452 AA.
AC P24379;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glycoprotein D precursor (Glycoprotein 17/18).
GN GD OR GP17/18 OR 72.
OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1), and
OS Equine herpesvirus type 1 (strain Kentucky D) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
CC NCBI_TaxID=31520, 10330;
CX [1]
RN RN SEQUENCE FROM N.A.
RP STRAIN=AB4p;
RC MEDLINE=9229556; PubMed=1318606;
RA Telford B.A.R., Watson M.S., McBride K., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-1.",
RT Virology 189:304-316 (1992).
RN RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=Kentucky D;
RC MEDLINE=91108393; PubMed=2177089;
RA Audomert J.-C., Wierslow J., Allen G., Paolletti E.;
RT "Equine herpesvirus type 1 unique short fragment encodes
RT glycoproteins with homology to herpes simplex virus type 1 gp, gI and
RT gE.",
RT J. Gen. Virol. 71:2969-2978 (1990).

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CC CC -1 SIMILARITY: Belongs to the herpesviruses glycoprotein D family.
CC -1 CAUTION: It is uncertain whether Met-1 or Met-51 is the initiator.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M6664; AAB02507.1; -.
CC DR PIR: I36802; VGBEG3.
CC DR InterPro: IPR002896; Herpes_glycop_D.
CC DR InterPro: IPR007110; Ig-like.
CC Pfam: PF01537; Herpes_glycop_D; 1.
CC Glycoprotein; Signal; Transmembrane.
CC SIGNAL 1 19 POTENTIAL.
CC CHAIN 20 452 GLYCOPROTEIN D.
CC DOMAIN 20 405 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 406 422 POTENTIAL.
CC DOMAIN 423 452 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 452 AA; 51099 MW; CF51E914F7F2E9DC CRC64;

Query Match 8.9%; Score 76.5; DB 1; Length 452;
Best Local Similarity 26.0%; Pred. No. 3.1;
Matches 44; Conservative 16; Mismatches 62; Indels 47; Gaps 8;

QY 2 KGTATLFLMTLIPSCSGGGGKAMPYHVCSDSLGVLYGSCDPLQDFGSVEKSKQ 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 161 KTSARL-TWFKIMPTC-----ATPIH-----DVSVMKCNPKLSFAMCDE----- 199
QY 62 LKSNINIRFGII--LRDIKELFLDLALMSGSSVL-----NFSYPICEAA 105
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 200 -RSDILMQASLTMAAETDDELGLVLAAPASASGLRYRIETIDGRQIYTDTSVTIPSER 258
QY 106 LP-----KFSFGGRKGEQIYVAGPVNN---PEFTIPQGEYVLTLELY 145
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 259 CPIAFEQNGNPDRCKTPEQYSRGEVFTRRFLGSEFNPQGEHMTWLKFW 307

RESULT 13
MURG_CAMUJ STANDARD; PRT; 342 AA.
ID MURG_CAMUJ STANDARD; PRT; 342 AA.
AC Q9PQ02;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UDP-N-acetylglucosamine--N-acetylmuramyl--(pentapeptide)
DE pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
DE (EC 2.4.1.227) [Undecaprenyl-PP-MurNAc-pentapeptide-UDP:GlcNAc
DE transferase].
GN MURG OR CJI039.
RN RN Campylobacter jejuni.
OS Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Bacteriobacteriaceae; Campylobacter.
CX NCBI_TaxID=197;
RN RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=NCTC 11168;
RC MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.W., Feltham T., Holtroyd S.,
RA Jagsi K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrall B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.",
RT Nature 431:665-668 (2000).

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CC - FUNCTION: Cell wall formation. Catalyzes the transfer of a GlcNAc
CC substrate on undecaprenyl-pyrophosphoryl-MurNAc-pentapeptide (lipid
CC intermediate I) to form undecaprenyl-pyrophosphoryl-MurNAc-
CC (pentapeptide)GlcNAc (lipid intermediate II) (By similarity).
CC CATALYTIC ACTIVITY: UDP-N-acetylglucosamine + Mur2Ac(oyl-L-Ala-
CC gamma-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol = UDP +
CC GlcNAc-(1->4)-Mur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)-
CC diphosphoundecaprenol.
CC - PATHWAY: Peptidoglycan biosynthesis; last step.
CC - SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
CC - SIMILARITY: Belongs to the glycosyltransferase family 28. MurG
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AI139077; CAB73295.1; -.
DR PIR: D81306; D81306.
DR HAMAP: MF_00033; -; 1.
DR InterPro: IPR007235; Glyco_tran_28_C.
DR InterPro: IPR004276; Glyco_tran_28.
DR InterPro: IPR006009; MurG.
DR Pfam: PF04101; Glyco_tran_28_C.1.
DR Pfam: PF03033; Glyco_tran28; 1.
DR TIGRfam: TIGR01133; murG.1.
DR Transferase: Glycosyltransferase, Cell division; Cell wall; Membrane;
DR Inner membrane; Peptidoglycan synthesis; Complete proteome.
DR SQ: SEQUENCE 342 AA; 38683 MW; F7013187068E9E7 CRC64;

Query Match 8.8%; Score 75.5; DB 1; Length 342;
Best Local Similarity 25.7%; Pred. No. 2.8; Indels 51; Gaps 11;
Matches 37; Conservative 22; Mismatches 34;

QY 35 DSGLEVLVYQSCDPLQDFGSVEKSKQLSKNINIR-----FGILLREDIKELFLDLALMS 89
DB 196 EQNKILIHQ_CGR-NDF-----EKCKGHYOS-INTQADIFDFSLNLEKKKN--ADLAISR 246
QY 90 QGSSVNFSEYFICEALP-----KF-----SFCGRKGEQIYYAGPIN 127
DB 247 AGASTL--FELCANTLPTFTFYPAAKKHQYFAKFLQDQALC-----QIFMONSIN 297
QY 128 NPEFTIPQGEYQVLELYTEKST 151
DB 298 LDEF-----FKSIKLNLNENIST 315

RESULT 14
PROB: CLOAB STANDARD; PRT; 1241 AA.
ID PROB: CLOAB STANDARD; PRT; 1241 AA.
AC C97EG9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
DE beta chain) (RNA polymerase beta subunit).
GN RPOB OR CAC3143.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1486;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=1146286;
RA Neelings J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tetunov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.,
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RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838 (2001).
CC - FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates.
CC - CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(n).
CC - SUBUNIT: The enzyme consists of the sigma chain and the core
CC enzyme which is composed of 2 alpha chains, 1 beta chain, and 1
CC beta' chain.
CC - SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC -----
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CC -----
DR EMBL: AE007809; AAK1081.1; -.
DR PIR: F97286; F97286.
DR InterPro: IPR007121; RNA_pol_B.
DR InterPro: IPR007644; RNA_pol_Rpb2_1.
DR InterPro: IPR007642; RNA_pol_Rpb2_2.
DR InterPro: IPR007645; RNA_pol_Rpb2_3.
DR InterPro: IPR007120; RNA_pol_Rpb2_6.
DR InterPro: IPR007641; RNA_pol_Rpb2_7.
DR Pfam: PF04563; RNA_pol_Rpb2_1.1.
DR Pfam: PF04561; RNA_pol_Rpb2_2.2.
DR Pfam: PF04565; RNA_pol_Rpb2_3.1.
DR Pfam: PF00562; RNA_pol_Rpb2_6.1.
DR Pfam: PF04560; RNA_pol_Rpb2_7.1.
DR PROSITE: PS01166; RNA_POL_BETA.1.
DR Transferase: Transcription; DNA-directed RNA polymerase;
DR Complete proteome.
DR SQ: SEQUENCE 1241 AA; 139248 MW; DEA50BA38BC4CB78 CRC64;

Query Match 8.8%; Score 75.5; DB 1; Length 1241;
Best Local Similarity 19.3%; Pred. No. 14;
Matches 29; Conservative 42; Mismatches 38; Indels 41; Gaps 9;

QY 35 DSGLEVLVYQSCDPLQDF-----GGSVEKSKSQ--LKSNNINIRGII 73
DB 40 DNGLOEIFDDINPQDYTGNIIEFYGKLDMDNIRKYSVECKERTTYAAPLKVQRLL 99
QY 74 LRE--DIK--ELFL-DIALMS-QGSSVNFSEYFICEALP-----SFCGRKGEQIYY 122
DB 100 NKEGVEYGEVFGDFPLMTBQGTFLNGAERTVSGVLRSPAYVDYIVDKKXKLLFS 159
QY 123 AGVYNNPEFTIPQGEYQVLELYTEKSTV 152
DB 160 ATVIEN-----RGAM--LEYETDSNSVI 180

RESULT 15
PROB: HUMAN STANDARD; PRT; 522 AA.
ID PROB: HUMAN STANDARD; PRT; 522 AA.
AC Q16Z22;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE UDP-N-acetylhexosamine pyrophosphorylase (Antigen X) (AGX) (Sperm-
DE associated antigen 2) [Includes: udp-N-acetylglactosamine
DE pyrophosphorylase (EC 2.7.7.2) (AGX-1); UDP-N-acetylglucosamine
DE UDP-N-acetylglucosaminylase (EC 2.7.7.23) (AGX-2)].
GN UAP1 OR SPAG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

RP SEQUENCE FROM N.A. (ISOFORM AGX1 AND AGX2).
 RC TISSUE=Testis;
 RX MEDLINE=94297079; PubMed=8025165;
 RA Diekmann A.B., Goldberg E.;
 RT "Characterization of a human antigen with sera from infertile patients."
 RL Biol. Reprod. 50:1087-1093(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM AGX1).
 RC TISSUE=Testis;
 RX MEDLINE=98269105; PubMed=9603950;
 RA Mito T., Yabe T., Arita M., Yamada-Okabe H.;
 RT "The eukaryotic UDP-N-acetylglucosamine pyrophosphorylases: gene cloning, protein expression, and catalytic mechanism."
 RL J. Biol. Chem. 273:14392-14397(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (AGX1/AGX2), PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RC TISSUE=Breast cancer;
 RX MEDLINE=98438464; PubMed=9765219;
 RA Wang-Gilliam A., Pastuszak I., Eibeln A.D.;
 RT "A 17-amino acid insert changes UDP-N-acetylhexosamine pyrophosphorylase specificity from UDP-GalNAc to UDP-GlcNAc."
 RL J. Biol. Chem. 273:27055-27057(1998).
 CC -1- FUNCTION: AGX1 converts GalNAc-1-P into UDP-GalNAc of UDP. AGX2 catalyzes the synthesis of GlcNAc-1-P into UDP-GlcNAc in the presence of UDP.
 CC -1- CATALYTIC ACTIVITY: UDP + N-acetyl-alpha-D-glucosamine 1-phosphate = diphosphate + UDP-N-acetyl-D-glucosamine.
 CC -1- PATHWAY: UDP-GlcNAc biosynthesis from Fru-6-P; fourth (last) step.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. IN SPERMATOZOEA, LOCALIZED TO THE PRINCIPAL PIECE OF THE TAIL, THE NECK REGION OF THE HEAD AND TO A LESSER EXTENT, THE MIDDLE PIECE OF THE TAIL.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=AGX2; Synonyms=AGX-2;
 CC IsoId=Q16222-1; Sequence=Displayed;
 CC Name=AGX1; Synonyms=AGX-1;
 CC IsoId=Q16222-2; Sequence=VSP_004483;
 CC -1- TISSUE SPECIFICITY: Widely expressed. AGX1 is more abundant in testis than AGX2, while AGX2 is more abundant than AGX1 in somatic tissue. Expressed at low level in placenta, muscle and liver.
 CC -1- DISEASE: ANTIGEN IMPLICATED IN ANTIBODY-MEDIATED MALE INFERTILITY.
 CC -----
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 CC -----
 CC EMBL; S73498; AAB31210.2; -;
 DR EMBL; AB011004; BAA31202.1; -;
 DR PDB; 1JVL; 28-AUG-02.
 DR PDB; 1JVG; 28-AUG-02.
 DR PDB; 1JVD; 29-AUG-02.
 DR PDB; 1JVG; 30-AUG-02.
 DR Genew; HGNC:12457; UAP1.
 DR MIM; 602862; -;
 DR GO; GO:0003977; F:UDP-N-acetylglucosamine diphosphorylase act. .; TAS.
 DR GO; GO:0006048; P:UDP-N-acetylglucosamine biosynthesis; TAS.
 DR InterPro; IPR002618; UDPGP.
 DR Pfam; Pf01704; UDPGP; 1
 DR Transferrase; Nucleosidytransferase; Antigen; Alternative splicing;
 KM Polymorphism; 3D-structure.
 FT SITE 111
 FT ACT SITE 115
 FT ACT SITE 122
 FT VASPLIC 454 470
 FT
 FT BINDING SITE FOR HEXNAC-1-P
 FT (BY SIMILARITY).
 FT POTENTIAL.
 FT POTENTIAL.
 FT Missing (in isoform AGX1).
 FT /FtId=VSP_004483.

FT VARIANT 418 418 P -> H (in dbSNP:1128539).
 FT FT /FtId=VAR_014935.
 FT CONFLICT 454 454 MISSING (IN REF. 1).
 SQ SEQUENCE 522 AA; 58840 MW; C823A9AD8659A135 CRC64;
 Query Match 8.7%; Score 75; DB 1; Length 522;
 Best Local Similarity 23.7%; Pred. No. 5.4;
 Matches 28; Conservative 19; Mismatches 35; Indels 36; Gaps 6;
 QY 27 WPTHTVCSDSGLVLYQSCPLQDFGFSVER---CSKQL--KSNINIRFGLIRED---- 77
 DB 245 WSHVYCVDM---ILTVVADP-RFIFGCIQKGDGAKVKEKTPPEPVGVCRVGVYQ 300
 QY 78 -IKELFLDLMSQSSVINFSPYDICEALPKTFCGRKGEQIYYAGPVNNPFTIP 134
 DB 301 VVEISEISLATQKRS-----DGRLLFNAGNIANNFTTVP 336

Search completed: April 29, 2004, 15:24:51
 Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 29, 2004, 15:21:06 ; Search time 41 Seconds
(without alignments)
1246.682 Million cell updates/sec

Title: US-09-899-917-2
Perfect score: 862
Sequence: 1 MKGPTATLFLWTILFPSCG.....ELYTEKRSTVACANATIMCS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :

SPRMBML_25:*
1:  sp_archaea.*
2:  sp_bacteria.*
3:  sp_fungi.*
4:  sp_human.*
5:  sp_invertebrate.*
6:  sp_mammal.*
7:  sp_mhc.*
8:  sp_organelle.*
9:  sp_phage.*
10: sp_plant.*
11:  sp_rodent.*
12:  sp_virus.*
13:  sp_vertebrate.*
14:  sp_unclassified.*
15:  sp_virus.*
16:  sp_bacterioph.*
17:  sp_bacterioph.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	115	13.3	160	6	Q8MT01	Q8MT01 oryctolagus
2	99	11.5	1197	16	Q82196	Q82196 arabidopsis
3	83	9.6	204	16	Q7RTM5	Q7RTM5 prochloroc
4	83	9.6	140	10	Q8LV30	Q8LV30 arabidopsis
5	81	9.6	466	17	Q58068	Q58069 pyrococcus
6	79.5	9.2	484	10	Q9S1N9	Q9S1N9 arabidopsis
7	79	9.2	2786	5	Q9SV02	Q9SV02 dirosophila
8	78	9.0	1133	3	Q12139	Q12139 saccharomyc
9	78	9.0	2409	17	Q960G6	Q960G6 dirosophila
10	77.5	9.0	394	15	Q9UY77	Q9UY77 pyrococcus
11	77.5	9.0	428	10	Q23839	Q23839 brassica o1
12	77	8.9	246	16	Q8ZB93	Q8ZB93 yersinia pe
13	77	8.9	396	5	Q76660	Q76660 toxoplasma
14	77	8.9	480	13	Q7ZT87	Q7ZT87 fugu rubrip
15	77	8.9	739	10	Q9MG64	Q9MG64 arabidopsis
16	77	8.9	751	10	Q8RV06	Q8RV06 arabidopsis

17	77	8.9	752	10	Q9A16	Q09A16 arbidopsi
18	76.5	8.9	404	5	Q0250	Q0250 caenorrhabi
19	76.5	8.9	262	12	Q04245	Q04245 equine heip
20	76.5	8.9	426	10	Q881D7	Q881D7 oryza sati
21	76.5	8.9	437	5	Q23653	Q23653 caenorrhabi
22	76.5	8.9	471	10	Q9MA46	Q9MA46 arbidopsi
23	76.5	8.9	1177	16	Q81V78	Q81V78 bacillus ari
24	76.5	8.9	1177	16	Q81J58	Q81J58 bacillus ce
25	76	8.8	303	10	Q8W4X5	Q8W4X5 lycopersic
26	76	8.8	670	10	Q8GX23	Q8GX23 arbidopsi
27	75.5	8.8	534	10	Q8RM76	Q8RM76 arbidopsi
28	75.5	8.8	1215	10	P93750	P93750 arbidopsi
29	75	8.7	377	6	Q46493	Q46493 bos tauru
30	75	8.7	505	4	Q96GM2	Q96GM2 homo sapien
31	75	8.7	699	10	Q9X196	Q9X196 arbidopsi
32	74.5	8.6	448	5	Q21761	Q21761 caenorrhabi
33	74.5	8.6	691	10	Q7XN01	Q7XN01 oryza sati
34	74	8.6	374	6	Q9T7M0	Q9T7M0 bos tauru
35	74	8.5	680	5	Q8WSN8	Q8WSN8 caenorrhabi
36	73.5	8.5	340	11	Q8RI13	Q8RI13 mus musculi
37	73.5	8.5	481	16	Q97D30	Q97D30 clostridiun
38	73.5	8.5	601	11	Q8PCF9	Q8PCF9 ratu
39	73	8.5	995	11	Q8X2R3	Q8X2R3 mus musculi
40	73	8.5	1106	16	Q92H19	Q92H19 ricketesia
41	73	8.5	98H19	5	Q98H19	Q98H19 drosophila
42	72.5	8.4	282	16	Q9ED173	Q9ED173 yersinia p
43	72.5	8.4	314	16	Q7VH15	Q7VH15 helicobact
44	72.5	8.4	553	16	Q8ED56	Q8ED56 shewanella
45	72.5	8.4	804	6	Q29113	Q29113 sus scrofa

ALIGNMENTS

RESULT 1			
ID	QEM101	PRELIMINARY;	PRT; 160 AA.
AC	QEM101;		
DT	01-OCT-2002 (TREMBLrel. 22, Created)		
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	MD-2.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_Taxid=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kajikawa O., Frevert C.W., Martin T.R.;		
RT	"Molecular cloning of rabbit MD-2,"		
RL	Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AY101395; AAM5061.1; "-		
DR	InterPro: IPR003172; E1.Derp2_Derp2.		
DR	InterPro: IPR007110; Ig-like		
DR	Pfam: PF02221; E1.Derp2_Derp2; 1.		
DR	SMART; SM00737; ML; 1.		
SQ	SEQUENCE 160 AA; 18186 MW; A2C1E0BA6E762F43 CRC64;		
Query March 13.3%; Score 115; DB 6; Length 160;			
Best Local Similarity 25.4%; Pred. No. 0.00027;			
Matches 35; Conservative 26; Mismatches 65; Indels 12; Gaps 4			
QY	30 HVCVCSGSEVLVYQSCDPLQ-DFGFVSEKSCSKQKNSINIRFGILREDIKELFLDLALM 88		
DB	22 HWCKSLADATVSTYCDNNEIPISINVEPCITLKGTLGHLHIFYPIDRMNOLYLNLYI- 80		
QY	89 SQGSAVLNFSYP-----ICFALLPFFSTCGRRKEGQIYVAGPVNPNPEFTIPQSEYQVLTLE 143		
DB	81 ----SVNSMDLPGRKEEILICKGSDVDVSEFCRALKGIVNTVTVPFSFKGIRLSKQYRCVVE 136		
QY	144 -LYTEKRSITVACANATIM 160		
DB	137 AIMGSAEMIFCLNPTTII 154		

RESULT 2
ID 082196 PRELIMINARY; PRT; 1137 AA.
AC 082196;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Copia-like retroelement pol polypeptin.
GN ATG519840.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldlyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanden S.E., Unayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RT Nature 402:761-768(1999).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
EMBL: ACO05169; AAC62132.1; -.
DR EMBL; G84581; G84581.
DR PIR; G84581; G84581.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006510; F:DNA recombination; IEA.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00098; zf_CCHC; 1.
DR PRINTS; PRO0393; CCHCNFINGER.
DR SMART; SMO0343; Znf_CCHC; 1.
DR PROSITE; PS00186; ZF_CCHC; 1.
KW Polypeptin.
SQ SEQUENCE 1137 AA; 129775 MW; 7265DF09C6E1025C CRC64;
Query Match 11.5%; Score 99; DB 10; Length 1137;
Best Local Similarity 26.3%; Pred. No. 0.15;
Matches 36; Conservative 23; Mismatches 42; Indels 36; Gaps 7;
QY 10 LMTLIPSCSG-----GGGKAMPTHYVCSGLFVLYQSCDPLQDGFSEV---55
DB 448 LMTSAVNPFGLKRFQGVVYVYSGEGLDPR---AKKGVFVG---PVGVGFFVMMI 499
QY 56 --EKCSQOLSNINIRGIIREDIKELFLDLALMSQSSVLNFSYPICAAALPKFSFCG 113
DB 500 EERCS-----ISRNVPREDV--MYKD--ILNSTGSMSPDLFLANRIPFECAG 547
QY 114 RRKGEQIYVAGPVNNPE 130
DB 548 NRKEDISVQGVSDDD 564

DE Possible occuludin/ELL family.
GN PMT1867.
OS Prochlorococcus marinus (strain Mtr 9313).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642;
RA Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land W., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
RT Nature 424:1042-1047(2003).
RL Nature 424:1042-1047(2003).
DR EMBL; BX572100; CAE22042.1; -.
KW Complete proteome.
SQ SEQUENCE 204 AA; 22142 MW; 6515E9FBDCE2D70A CRC64;
Query Match 9.6%; Score 83; DB 16; Length 204;
Best Local Similarity 24.2%; Pred. No. 1;
Matches 37; Conservative 22; Mismatches 36; Indels 58; Gaps 9;
QY 13 LIP-SCSGGGKAMPTHYVCSGLF-----VLYSCDPLQDGFSEVCKSK 60
DB 36 LVTPLAVTGMGGGLAMPVVCITL-LEAPDANOSKGPVEVQCGPLSTGLIER--- 91
QY 61 QLKSNINIRF-----GIIREDIKELFLDLALMSQ-GSSVLNFSYPICAAALPKFS 110
DB 92 -----RFSWAPVPGVDVLHQLTM-LGIAVAGGGRNLMGFRP----- 132
QY 111 FCGRRKGEQIYVAGPVNNPEPTIPGEYVILE 143
DB 133 -----DQTIIMDG-----SAVNTYQVILE 152
RESULT 4
QY 09LV30 PRELIMINARY; PRT; 1440 AA.
AC 09LV30;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE EMBL; CAB40755.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl.
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AB020749; BAB02023.1; -.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PRO1535; PPR; 25.
DR TIGRNAME; TIGR00756; PPR; 24.
SQ SEQUENCE 1440 AA; 162336 MW; 364887F23EF8B9BF CRC64;
Query Match 9.6%; Score 83; DB 10; Length 1440;

Best Local Similarity 22.5%; Pred. No. 11;
Matches 27; Conservative 22; Mismatches 57; Indels 14; Gaps 3;

QY 30 HVCVSDSGLEVLVYQSCDPLQDFGFSVEKSKQKSNINIRFGIILREDIKELFLDLALMS 89
DB 830 HALCVDRLEELVYVVEELQDWGFKSKSILMLDAFAGNIF--EVKXIYSSMKAA 887
QY 90 QSSVYNFSEYPI---CEALPKFSCGRKGEQIYAGVNNPEFTIQGEYQVLELYT 146
DB 888 YIPTRILYMMTELLCK-----GKKVDAEIVISEMERANKVELAINSMKQYT 938

RESULT 5

OS08069 PRELIMINARY; PRT; 406 AA.

AC OS08069; PRELIMINARY; PRT; 406 AA.
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein PH0331.
GN PH0331.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Chikui Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000002; BAA29405.1; -.
DR PIR; H71139; H71139.
DR InterPro; IPR002881; DUF58.
DR Pfam; PF01882; DUF58; 1.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 406 AA; 45912 MW; 694855F337C5DD8D CRC64;

Query Match 9.4%; Score 81; DB 17; Length 406;
Best Local Similarity 25.8%; Pred. No. 3.8;
Matches 39; Conservative 27; Mismatches 49; Indels 36; Gaps 9;

QY 1 MKG--FTATLFLWTLTFPSGSGGGGKA-WPTHVCSDSGLVLYQSCDPLQDFG--SV 55
DB 4 MKGASFFVTLFLFVMSLTFVPGKLAFFLLLT---VGLLF--DAGDFEYVERI 56
QY 56 EKC-----SKQKSNINIRFG-----ILREDIKELFLDLALMSQSSVYNFSPICEAAL 106
DB 57 EKQRTFVGNIEVLVAVRGIGLVVRENIPKAF-----MSSGSNVYF----- 103
QY 107 PKTSFCGRKGEQIYAGVNNPEFTIQGE 137
DB 104 --FTYGRSFSQSLPLPKRGVYELPKTE 132

RESULT 6

OS08199 PRELIMINARY; PRT; 484 AA.

AC OS08199; PRELIMINARY; PRT; 484 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative triacylglycerol lipase.
GN AT2G31690.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldguy T.V.,
RA Buell C.R., Ketchum K.A., Lee J.-U., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanden S.E., Umeyan L., Jallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Scriver C.R.,
RA Salzman S.L., Fraser C.M., White O., Eisen J.A.,
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RT Nature 402:761-768(1999).
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007071; AAD24845.1; -.
DR PIR; H84723; H84723.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR002921; Lipase_3.
DR InterPro; IPR00379; Ser esters.
DR Pfam; PF01764; Lipase_3; 1.
SQ SEQUENCE 484 AA; 54923 MW; 74650CD21B878303 CRC64;

Query Match 9.2%; Score 79.5; DB 10; Length 484;
Best Local Similarity 27.4%; Pred. No. 6.8;
Matches 34; Conservative 18; Mismatches 43; Indels 29; Gaps 5;

QY 35 DSGLEVLVYQSCDPLQDFGFSVEKSKQKSNINIRFGIILREDIKELFLDLALMSQSSV 94
DB 248 ESGFLSLYTSDESSKGG--LESRCQLSEIS---RLMKYKGEHSITLACHSMSSSL 302
QY 95 LNFSPYICEMALPK-----FSPGRRKGE-----QIYAGPVNPE 130
DB 303 AQLAYDAIEGLNRRICKGDIPTVTFSPAGPVGNIEFKRGEELGVKTLRTNVDPV 362
QY 131 FTIP 134
DB 363 TKLP 366

RESULT 7

OSVSU2 PRELIMINARY; PRT; 2786 AA.

ID OSVSU2; PRELIMINARY; PRT; 2786 AA.
AC OSVSU2; OSVSU2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CG4821 protein.
GN TEOUHLA OR CG4821 OR CG4948 OR CG18403.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutcliffe G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer J.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA April J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandal D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.B., Domes W., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.B., Gary N.S., Gelbart W.M., Glaserman W.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Palazolo M., Pittman K.A., Nixon K., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of *Drosophila melanogaster*.";
 RA Science 287:2185-2195(2000).
 RA [2]
 RA SEQUENCE FROM N.A.
 RA Centner S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Bazon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champagne M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferrera S., Frisze E., Galle R.F., Gary N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,
 RA Paclet J., Paradas V., Park S., Patel S., Pfeiffer B.,
 RA Prounauvong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
 RA "Sequencing of *Drosophila melanogaster* genome.";
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RA [3]
 RA SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Procinis S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Centner S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frisze E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RA "Annotation of *Drosophila melanogaster* genome.";
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RA [4]
 RA SEQUENCE FROM N.A.
 RA Adams M.D., Centner S.E., Gibbs R.A., Rubin G.M., Venter J.C.,
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RA [5]
 RA SEQUENCE FROM N.A.
 RA FlyBase;
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RA CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 51.
 RA EMBL; AF003553; AAF50319.3; -
 RA HSP; P00750; IRTF.
 RA FlyBase; FBgn0023479; Tegula.
 RA GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008061; F:chitin binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0005044; F:scavenger receptor activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006030; P:chitin metabolism; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR GO; GO:0015992; P:proton transport; IEA.
 DR InterPro; InterPro0194; ATPase_a/bcentre.
 DR InterPro; InterPro02557; Chitin_Bind_Perf.
 DR InterPro; InterPro09003; Cys_Ser_Trypsin.
 DR InterPro; InterPro02172; LDL_receptor_A.
 DR InterPro; InterPro01254; Peptidase_S1.
 DR InterPro; InterPro01314; peptidase_S1A.
 DR InterPro; InterPro01190; Strc_receptor.
 DR Pfam; PF01607; CBM_14; 15.
 DR Pfam; PF00530; SRCR_2.
 DR Pfam; PF00530; SRCR_2.
 DR Pfam; PF00530; SRCR_2.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00261; LDLRECEPTOR.
 DR PRINTS; PR0258; SPERACTRPT.
 DR SMART; SM00494; ChEBD2; 15.
 DR SMART; SM00192; LDLA; 2.
 DR SMART; SM00202; SR; 2.
 DR SMART; SM00202; Tryp_Spc; 1.
 DR PROSITE; PS00105; ATPase_ALPHA_BETA; 1.
 DR PROSITE; PS01209; LDLR_1; 1.
 DR PROSITE; PS00068; LDLR_2; 2.
 DR PROSITE; PS00420; SRCR_1; 2.
 DR PROSITE; PS0287; SRCR_2; 2.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Protease; Serine protease.
 DR SEQUENCE 2786 AA; 308362 MM; 28ED7A7DA5002C76 CRC64;
 SQ
 Query Match 9.2%; Score 79; DB 5; Length 2786;
 Best Local Similarity 26.9%; Pred. No. 63;
 Matches 28; Conservative 20; Mismatches 36; Indels 20; Gaps 6;
 QY 12 TLIFSCGGGGG-KAMP-----THVCSDSGLTLYGSCDPLQDFGSVKKC--SKQLKS 64
 DB 770 TWLSACPDGNGHLHYDAGKTVRCSDG-KNISTGCEQNAFSLGACRPSRLIST 828
 QY 65 NINIFGILLREDI-----KELFDLALMSGSSVYNFSYP 100
 DB 829 EDRVRF-----RELQIQTVSSODIQIQSPDKCPSTLRGNYP 868
 RESULT 8
 ID Q12139 PRELIMINARY; PRT; 1133 AA.
 AC Q12139;
 DT 01-NOV-1996 (TrEMBLrel. 01. Created)
 DT 01-NOV-1996 (TrEMBLrel. 01. Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24. Last annotation update)
 DE yPro22C protein.
 GN yPro22C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB972;
 RA Badcock K., Bowman S., Churcher C.M., Pearson D., Rajandream M.A.,
 RA Walsh S.V., Barrett B.G.;
 RA Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=AB972;
 RA Badcock K., Chaurcher C.M.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB972;
 RA Barrett B., Rajandream M.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 271255; CAA95018.1; -
 DR EMBL; 249274; CAA99276.1; -
 DR PIR; S54496; S54496.
 DR SGD; S0006226; YPR022C.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; Zf-C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 2.
 DR Hypothetical protein; Metal-binding; Zinc; zinc-finger.
 KW SEQUENCE 1133 AA; 130116 MW; 77F63C9E3760DA CRC64;

Query Match 9.0%; Score 78; DB 3; Length 1133;
 Best Local Similarity 25.3%; Pred. No. 27;
 Matches 37; Conservative 16; Mismatches 31; Indels 62; Gaps 8;

QY 46 DEVDHGFSEKES-----KQKLS--NINIRGII--LRDIE 80
 DB 472 DEPTKIKSEKQEMFPELRYVSIHSKLSFMINHPQGLHKSFYDKOP 531
 QY 81 LFLDLALMSGSSVLYNFY-----PCEALPKFSCGRKGEQIYVAPV--NNP 129
 DB 532 AINLNLIMTGASFLESEYREQISDPIC-----GPIRLWIFSHA 570
 QY 130 EFTIPGGEYGV-----LLELYTERST 151
 DB 571 DFQPPSKTYITQSLIIVEGY-EKTSST 595

RESULT 9

ID 096006 PRELIMINARY; PRT; 2409 AA.
 AC 096006;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE S02860P.
 GN TEQUILA OR CG4821 OR CG4948 OR CG18403.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brockstein P., Hong L., Agbayan A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Paclet J., Paragas V., Park S., Phocanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celisner S.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; AY052072; AK93496.1; -
 DR HSSP; P00761; IAN1.
 DR FlyBase; FBgn0023479; Tequila.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008061; F:chitin binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0005044; F:scavenger receptor activity; IEA.
 DR GO; GO:0004255; F:trypsin activity; IEA.
 DR GO; GO:0006030; P:chitin metabolism; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR GO; GO:0015992; P:proton transport; IEA.
 DR InterPro; IPR000194; ATPase_a/bcentre.
 DR InterPro; IPR002557; Chitin_Bind_Pera.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR002172; IDL_receptor_A.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR001190; Src_receptor.
 DR Pfam; PF01607; CBM_14; 10.
 DR Pfam; PF00057; Idl_recept_a; 2.
 DR Pfam; PF00530; SRCR; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00261; LDLRECEPTOR.
 DR PRINTS; PR00258; SPERACTRPT.
 DR SMART; SM00494; ChEBD2; 10.
 DR SMART; SM00192; LDLA; 2.
 DR SMART; SM00202; SR; 2.
 DR SMART; SM00020; Tryp_spc; 1.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
 DR PROSITE; PS01209; IDLRA_1; 1.
 DR PROSITE; PS00068; IDLRA_2; 2.
 DR PROSITE; PS00420; SRCR_1; 2.
 DR PROSITE; PS0287; SRCR_2; 2.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Protease; Serine protease.
 KW SEQUENCE 2409 AA; 267618 MW; 4F014411D0B87150 CRC64;

Query Match 9.0%; Score 78; DB 5; Length 2409;
 Best Local Similarity 26.0%; Pred. No. 68;
 Matches 27; Conservative 21; Mismatches 36; Indels 20; Gaps 6;

QY 12 TLIPSGCGGGG-KAMP-----THVGSGLGLVLYSCDPLDFGFSVEK--SKQLS 64
 DB 394 TWLSACPDGNGHLVYDAGKYVCSGG-KMSIQSCENQMAFSLQACRPSRLVST 452
 QY 65 NINIRFGIILREDI-----KELFLDLALMSGSSVLYNFY 100
 DB 453 EDNRVF-----RELDIQTYSQDIHQSPKCKPSVLRGNYP 492

RESULT 10

ID 09UY77 PRELIMINARY; PRT; 394 AA.
 AC 09UY77;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE PEPX related from CALDICEULLOSINUPTOR SACCHAROLYTICUS.
 GN PYRAB16310 OR PAB1277.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=GES / Orsay;
 RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 structure and evolution."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ246288; CAB50535.1; -
 DR PIR; A75012; A75012.
 DR InterPro; IPR002881; DUF58.
 DR Pfam; PF01882; DUF58; 1.
 KW Complete proteome.
 KW SEQUENCE 394 AA; 44831 MW; 39C29C86B1A95245 CRC64;

Query Match 9.0%; Score 77.5; DB 17; Length 394;
 Best Local Similarity 23.4%; Pred. No. 8.7;
 Matches 36; Conservative 31; Mismatches 44; Indels 43; Gaps 9;

QY 1 MKG--FTATLPLMTLIFPSCGGGGGSKA-WPTHVVCSDSGLEVLVYQSCDPLQDFGFSYK 57
 DB 1 MKGVSEFLTLFLMFLVSLVIFGTPKTLAFLPLIIT- - - - -VGMIDPT- - - - -PGGFTYER 51
 QY 58 - - - - -CSKOLKSNINIRFG- - - - -ILREDIKELFLDLALMSGSSVLN-PSYICE 103
 DB 52 EYTKRREVFVGESEYRVKLRVRSKGIIVILKENLPRAF- - - - -EYKSGATFFHFTYPCR 106
 QY 104 AALPKFSGCRGEGEIIYVAGPNNPEFTIPGE 137
 DB 107 ERFSEYSFVPRKRG- - - - -EYDIPKTE 128

RESULT 11

Q23839 PRELIMINARY; PRT; 428 AA.
 AC 023839;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE S glycoprotein (Fragment).
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OC NCBI_TaxID=3712;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97352858; PubMed=9207151;
 RA Kusaba M., Nishio T., Saita Y., Ockendon D.,
 RT "Striking sequence similarity in inter- and intra-specific comparisons
 of class I SLG alleles from Brassica oleracea and Brassica
 campestris: implications for the evolution and recognition
 mechanism".
 RL Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678 (1997).
 DR EMBL: D85205; BAA21939.1; -
 DR PIR: T14529; T14529.
 DR GO: GO:0005529; P=sugar binding; IRA.
 DR InterPro: IPR001480; B_lectin.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR000858; Slocus_glycop.
 DR Pfam: PF01453; Agglutinin_1.
 DR Pfam: PF00954; S locus glycop; 1.
 DR SMART: SM00108; B_lectin; 1.
 DR SMART: SM00473; Pan_AP; 1.
 FT NON_TER
 FT 428
 FT 428
 SQ SEQUENCE 428 AA; 48724 MW; 18E04542C7293BEA CRC64;

Query Match 9.0%; Score 77.5; DB 10; Length 428;
 Best Local Similarity 25.2%; Pred. No. 9.7;
 Matches 21; Conservative 20; Mismatches 49; Indels 11; Gaps 4;

QY 49 QDFGFSYKSKOLKSNINIRFGIILREDIKELFLDLALMSGSSVLNPSYICPALPK 108
 DB 149 QSFDFPDTLLPEMKAGYNLKTG- - - - -NRFLLTAMRNSDDPSSGDSYKLENNELPE 201
 QY 109 FSGCRKRGEOIYVAGPNNPEFT-IPGE-YOVLLLEYKRSSTVA 153
 DB 202 FYLL--KSGFQVHRSGWNGVRSGIPENOKLSYMTNFTNSEEVA 246

RESULT 12

Q8ZBY9 PRELIMINARY; PRT; 246 AA.
 AC 08ZBY9;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Putative exported protein.
 GN YP03241.
 OS Yersinia pestis

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OC NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Tildall R.W., Holden M.T.G.,
 RA Pringle M.B., Sebaiha M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Felwell T., Hamlin N., Holroyd S., Jagers K., Kariyasek A.V.,
 RA Leather S., Mout R., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,
 RT "Genome sequence of Yersinia pestis, the causative agent of plague".
 RL Nature 413:523-527 (2001).
 DR EMBL: AJ414156; CAC92476.1; -
 DR PIR: AH0393; AH0393.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 246 AA; 27994 MW; 83FAL4455C2F82BC CRC64;

Query Match 8.9%; Score 77; DB 16; Length 246;
 Best Local Similarity 29.0%; Pred. No. 5.6;
 Matches 31; Conservative 12; Mismatches 30; Indels 34; Gaps 6;

QY 45 CDFQDFGFSYK- - - - -CSKOLKSNIRFGIILREDIKELFLDLALMSGSSVLNPS 98
 DB 13 CLPASFTSSSEPVAVSKELKQGLGSSVYIIFKEREVLLEYAKL- - - - -QSEYRLVQS 68
 QY 99 YPICEALPKFSGFCG- - - - -RRKGEQIYVAGPNNPEFTIPGEYCV 140
 DB 69 YPICE- - - - -FSGGAGPKRREG- - - - -DFKSPGFTYR 96

RESULT 13

Q76660 PRELIMINARY; PRT; 396 AA.
 AC 076660;
 ID 076660;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Putative GPI-anchored surface antigen SRS4.
 GN SRS4.
 OS Toxoplasma gondii.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
 OC Toxoplasma.
 OC NCBI_TaxID=5811;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RH;
 RA Hehl A., Boothroyd J.C.;
 RT "SRS4, a member of the SAG1 family of surface antigens in Toxoplasma
 gondii".
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF078678; AAC27649.1; -
 DR InterPro: IPR007226; SAG.
 DR Pfam: PF04092; SAG; 1.
 DR PRINTS: PRO1801; SURFCANTIGN.
 SQ SEQUENCE 396 AA; 42105 MW; 7E96A39F44D15A02 CRC64;

Query Match 8.9%; Score 77; DB 5; Length 396;
 Best Local Similarity 21.1%; Pred. No. 10;
 Matches 37; Conservative 22; Mismatches 62; Indels 54; Gaps 6;

QY 24 GRAMPTHVVCSDSG- - - - -EVLVQSCDPLQDFGFSYKSKOLKSNINIR- - - - - 69
 DB 170 GEWTLQIQESDPLPLTKRAFVCGDNKAGAKDVQTSKCKCVFNKARPSFVAENNVV 229
 QY 70 - - - - -FGIILREDIKELFLDLALMSGSSVLNPSY 99
 DB 230 TCVAGKSNPEPLNVTMTNTLTITQCGSHGVLPYSYATFCDL- - - - -ODIMQKCTE 285
 QY 100 PICEALPKF- - - - -SFGCRKRGEOIYVAGPNNPEFTIPGEYOVLL- - - - -LYTEKSGT 151

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DB 286 KKEPILPSFTWANSKDQ--SATLTLEAFPEQSEQFRLSCYKAKOST 337

RESULT 14

07287 PRELIMINARY; PRT; 480 AA.

ID 07287; PRELIMINARY; PRT; 480 AA.
AC 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DS Nicotinic acetylcholine receptor beta 1b subunit (Fragment).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Jones A.K., Edgar G., Sattelle D.B.;
RT "The nicotinic acetylcholine receptor gene family of the pufferfish.
RT Fugu rubripes.";
RL Genomics 0:0-0(2003).
DR EMBL; AY299468; AAP58383.1; -.
KM Receptor.
FT NON TER
SQ SEQUENCE 480 AA; 55233 MW; D0CD232938E06C0 CRC64;

Query Match 8.9%; Score 77; DB 13; Length 480;
Best Local Similarity 29.9%; Pred. No. 13;
Matches 23; Conservative 14; Mismatches 24; Indels 16; Gaps 4;

QY 23 GCGAW-PTHVVCSDSGLEVLVYQSCDPLDPGSEVSKSKOLKS-----NINIRFGIILR 75
DB 115 GRVTWTPPALVYSCSGVKEY-----FFPDWNCMSQFRSYTYDSTEIDVQYALNLR 166

QY 76 -EDIKELFLDLALMSQG 91
DB 167 GQEIREFQIDAEAFTEG 183

RESULT 15

Q9M9G4 PRELIMINARY; PRT; 739 AA.

ID Q9M9G4; PRELIMINARY; PRT; 739 AA.
AC Q9M9G4;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE F14023.20 protein.
GN F14023.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RA Liu S., Yu G., Lee J., Sakano H., Chaveri A., Lenz C., Toriumi M.,
RA Chin C., Chlou J., Choi E., Gonzalez A., Hong B., Koo T., Li J.,
RA Liu A., Pham P., Vaysberg M., Altafi H., Buehler E., Chao Q., Conn L.,
RA Conway A.B., Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B.,
RA Nguyen M., Palm C., Shinn P., Tambunga G., Davis R., Ecker J.,
RA Federpriel N., Theologis A.;
RT "The sequence of BAC F14023 from Arabidopsis thaliana chromosome 1.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RA Theologis A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC012654; AAP43235.1; -.

DR PIR; G96740; G96740.
SQ SEQUENCE 739 AA; 84156 MW; 9EDASEEF888B8AB CRC64;

Query Match 8.9%; Score 77; DB 10; Length 739;
Best Local Similarity 24.0%; Pred. No. 21;
Matches 25; Conservative 17; Mismatches 30; Indels 32; Gaps 4;

QY 48 LDPGSEVSKSKOLKSINIRFGIILR--EDIKELFLDLALMSQSSVLYNFSYPCER 104
DB 264 VQKGRK-DKCYEQIRKAVDRNRLTLVFDLK-----A 298

QY 105 ALPKTFGCRKRGKQIYVAGPVNNPEFTIPQGEYVLELYTER 148
DB 299 ALPEARVIGELGDIYDVYAPCFPPRYEI----FQLMVNLVTER 338

Search completed: April 29, 2004, 15:23:13
Job time : 43 secs